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Q80YZ0
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Q90W79
Q90DZ5
Q40JSD9
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TN11 HUMAN
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| TANDARD; PRT; 281 A  34, Created) 34, Last sequence update 45, Last annotation update actor ligand superfamily m ng ligand) (TRAIL protein) nonyms=APOZL, TRAIL; man). (Chordata; Craniata; Ve ia; Primates; Catarrhini;  A. PubMed=86777713; DOI=10.1 chey K., Smolak P.J., Din therland G.R., Davis-Smith and characterization of a sptosis."; 82(1995).  A.  PubMed=8663110; DOI=10.1 ters S.A., Ruppert S., Don optosis by Apo-2 ligand, a cytokine family."; 1112687-12690(1996).  A.  PubMed=12477932; DOI=10.1 Feingold E.A., Grouse L.H. collins F.S., Wagner L., Sh eaberg B., Buetow K.H., Sc rdan H., Moore T., Max S. I lano N.A., Peters G.J., A ares M.B., Bonaldo M.F., C Usdin T.B., Toshiyuki S., lano N.A., Peters G.J., A ares M.B., Bonaldo M.F., C Usdin T.B., Toshiyuki S., lano N.A., Peters G.J., A lano N.A., Peters G.J., A lano N.A., Peters G.J., A lano N.A., Sodergren E.J., lano N.A., Sodergren E.J., lano N.A., Sodergren E.J., lano N., Young A.C., Shevchen Touchman J.W., Green E.D., nh, Young A.C., Shevchen Touchman J.W., Green E.D., initial analysis of more t   | TN14 HUMAN Q8MJ19 Q7T2Q3 TN14 MOUSE TNF5_CALJA TNF5_FELCA Q6UB17 TNF5_FELCA Q6UB17 TNF5_CANFA TNF5_CANFA TNF5_HUMAN Q70332 TNF5_PIG ALIGNMENTS                    |
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| ed<br>o-2L).<br>omi;<br>os7-0;<br>h C.A.,<br>NP family<br>tumor<br>tumor<br>tumor<br>tumor   | homo sapien macaca mula cyprinus ca mus culu callithrix actus trivi felis silve lateolabrax cercocebus macaca mula canis famil homo sapien mesocricetu sus scrofa |

mouse

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EMBL; U37518; AAC50332.1; -.
EMBL; U57059; AAB01233.1; -.
EMBL; BC032722; AAB13722.1; -.
PDB; 1D0G; X.ray; A/B/D=114-281.
PDB; 1D2Q; X.ray; A=114-281.
PDB; 1D4V; X.ray; B=119-281.
PDB; 1D4V; X.ray; B=119-281.
PDB; 1D4V; X.ray; B=119-281.
PDB; 1D4V; X.ray; D/E/F/J/K/L=114-281.
                                                                         MIM; 603598; ...
GO; GO:0005887; C:integral to plasma membrane; TAS.
GO; GO:0005625; C:soluble fraction; TAS.
GO; GO:0005625; F:receptor binding; TAS.
GO; GO:0005102; F:receptor binding; TAS.
GO; GO:0007267; P:cell-cell signaling; TAS.
GO; GO:00043123; P:positive regulation of I-kappaB kinase/NF-k.
GO; GO:00043123; P:positive regulation of I-kappaB kinase/NF-k.
GO; GO:00043123; P:positive regulation of I-kappaB kinase/NF-k.
GO; GO:0007165; P:signal transduction; TAS.
InterPro; IPR006052; TNF family.
InterPro; IPR006053; TNF family.
InterPro; IPR003636; TNF subf.
Pfam; PF00229; TNF; 1.
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"2.8 A
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ProDom; PD002012; TN
SMART; SM00207; TNF;
PROSITE; PS00251; TN
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MEDLLNE=99413670; PubMed=10485660; DOI=10.1016/S1074-7613(00)80100-4;
Cha S.-S., Kim M.S., Choi Y.H., Sung B.J., Shin N.K., Shin H.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jones E.Y., Screaton G.R.;
"Structure of the TRAIL-DR5 complex reveals specificity in apoptotic initiation.";
Nat. Struct. Biol. 6:1048-1053(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS)
PubMed=10542098; DOI=10.1038/14935;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 114-281.

MEDLLNE=20017054; PubMed=10549288; DOI=10.1016/S1097-2765(00)80207-5;

Hymowitz S.G., Christinger H.W., Fuh G., Ultsch M., O'Connell M.,

Kelley R.F., Ashkenazi A., de Vos A.M.;

"Triggering cell death: the crystal structure of Apo2L/TRAIL in a complex with death receptor 5.";

Mol. Cell 4:563-571(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        selective antitumor activity.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mongkolsapaya J., Grimes J.M., Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mmunity 11:253-261(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in fied and this statement is not removed. Usage by and for con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBUNIT: Homotrimer.
SUBCELLULAR LOCATION: Type II membrane protein (Potential).
TISSUE SPECIFICITY: Widespread; most predominant in spleen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: Cytokine that binds to TMFRSF10A/TRAILR1, TMFRSF10B/TRAILR2, TMFRSF10B/TRAILR3, TMFRSF10B/TRAILR4 possibly also to TMFRSF11B/OPG. Induces apoptosis. Its amay be modulated by binding to the decoy receptors TMFRSF10B/TRAILR4 and TMFRSF11B/OPG the second that the second the second that the second the second that the second th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: Belongs to the tumor necrosis factor family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         induce apoptosis.
COFACTOR: Binds 1 zinc
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l. Acad. Sci. U.S.A.
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Q8K3G0;
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                   STRAIN=DA;
Mueller A.M., Giegerich G.;
Submitted (MAY-2002) to the
EMBL; AVI15578; AAM49797.1;
HSSP; P50591; 1D20.
                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10116;
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TNF-related apoptosis inducing ligand.
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                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat).
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D-structure; Apoptosis; Cytokine; Metal-binding; Signal-anchor;
GO:0016020;
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Signal-anchor for type II
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F:tumor necrosis factor receptor binding;

IEA.

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RRESULT 3
TN10 MOUSE
ID TN10 M
AC P50592
DT 01-OCT
DT 01-OCT
DT 01-OCT
DT 01-OCT
DT 01-OCT
DT 01-OCT
DT 05-JUL
DE apopto
GN Name=T
OS MUS mu
OC Eukary
OC Mammal
OX NCBL_T
RN 111
RP SEQUEN
RA Wiley
RA Wiley
RA Wiley
RA Michol
RA Goodwi
RT that i
RI Immuni
CC -i- FU
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CC -i- SU
CC -i- SI
CC This S
CC This
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Best Local S
Matches 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO:0005164; F:tumor necrosis factor receptor bi:
GO; GO:0006955; P:timmune response; IEA.
R Interpro; IPR006052; TWF family.
R Interpro; IPR003636; TWF_1ike.
R Interpro; IPR003636; TWF_1ike.
R Interpro; IPR003636; TWF_subf.
R Pfam; PF00229; TWF; 1.
R ProDom; PD002012; TWF_subf; 1.
R PROSITE; PS00207; TWF; 1.
R PROSITE; PS00251; TWF 1; UNKNOWN_1.
R PROSITE; PS0049; TWF_2; 1.
R PROSITE; PS0049; TWF_2; 1.
CA4F5B5D7C833FEC CRC
                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

MEDLINE-96111955; PubMed-8777713; DOI
WILEY S.R., Schooley K., Smolak P.J.,
Nicholl J.K., Sutherland G.R., Davis-
Goodwin R.G.;
"Identification and characterization
                                                                                                                         that induces apoptosis.";

Immunity 3:673-682(1995).

-I-FUNCTION: Cytokine that binds to TNFRSF10A/TRAILR1,

TNFRSF10B/TRAILR2, TNFRSF10C/TRAILR3, TNFRSF10D/TRA

possibly also to TNFRSF11B/OPG. Induces apoptosis.

may be modulated by binding to the decoy receptors

TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and TNFRSF11B/
                                                                                                                                                                                                                                                                                                                                                                                                                                    p50592;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Tumor necrosis factor ligand superfamily member
apoptosis inducing ligand) (TRAIL protein).
                                                                                                                                                                                                                                                                                                                                                                      Name=Tnfsf10; Synonyms=Trail;
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                      induce apoptosis.
SUBUNIT: Homotrimer (By similarity).
SUBUNIT: Homotrimer (By similarity).
SUBCELLULAR LOCATION: Type II membrane protein (Potential TISSUE SPECIFICITY: Widespread.
TISSUE SPECIFICITY: Widespread.
SIMILARITY: Belongs to the tumor necrosis factor family.
SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cch 65.2%; Score 963; DE al Similarity 67.7%; Pred. No. 8.56 189; Conservative 29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YSQTYFRFQE--EIKENTKND----KQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQRVAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                          Davis-Smith T.,
                                                                                                                                                                                                                                                                       DOI=10.1016/1074-7613(95)90057-8;
.J., Din W.S., Huang C.-P.,
vis-Smith T., Rauch C., Smith C.A.
                                                                                                                                                              Induces apoptosis. Its
                                                                                                                                                                                                                                            of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      291
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.5e-71;
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                                                                                                                                                                               TNFRSF10D/TRAILR4
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                                                                                                                              receptors
TNFRSF11B/OPG
                                                                                                                                                                                                                                              member
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                                                                                 (Potential).
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                                                                                                                                                                                                                                              the
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Best Local S
Matches 177
                                                                                                                                                                                                                 Q7T1F2;
Q7T1F2;
01-OCT-2003
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
CARBOHYD
SEQUENCE
                                                                                                                                     Gallus gallus (Chicken).
Eukaryota; Metazoa; Chor
Archosauria; Aves; Neogn
                                                                                                                                                                                     01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Tumor necrosis factor related apoptosis inducing ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ProDom; PD002012; TNF subf; 1.

SMART; SM00207; TNF; I.

PROSITE; PS00251; TNP_1; 1.

PROSITE; PS00251; TNP_2; 1.

Apoptosis; Cyrokine; Signal-anchor; Transmembrane.

Apoptosis; Cyrokine; Signal-anchor; Doubain 1 17

TRANSMEM 18 38 Signal-anchor; Tpor type II
Sayed A.A., Horiuchi H., Furusawa "Molecular Cloning and Characteriz Factor (TNP)-Superfamily Ligands, Inducing Ligand (TRAIL).";
J. Vet. Med. Sci. 66:43-650(2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                         TISSUE=Spleen;
                                                                                      SEQUENCE FROM
                                                                                                             NCBI_TaxID=9031;
                                                                                                                                                                                Name=TRAIL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGD; MGI:107414; Thf8f10.
InterPro; IPR006052; TNF family.
InterPro; IPR008983; TNF like.
InterPro; IPR003636; TNF subf.
Pfam; PF00229; TNF; 1.
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177; Conserv
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DASKMVSKDKVRTKQLVQYIYKYTSYPDPIVLMKSARNSCWSRDAEYGLYSIYQGGLFEL
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                                                                                                                                                                                                                                                                                                                    KKNDRIFVSVTNEHLMDLDQEASFFGAFLI
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                                                                                                                                                                                                                                                       PRELIMINARY;
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52
                                                                                      N.A.
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52
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                                                                                                                                      Neognathae;
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Neognathae; Galliformes; Phasianidae; Phasiani
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                                   Characterization
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Pred. No. 4.4e-68;
7; Mismatches 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein (Potential).
Extracellular (Potential)
N-linked (GlcNac. . .) (Potential)
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                                      Matsuda H.;
on of Chicken Tumo
OL and TNF-Related
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RESULT
Q6DHG9
ID Q6DHG9
ID Q6
AC Q6

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MEDILIBE-2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
XX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
XX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
XX Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
XX Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
XX Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
XX Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
XX Altochenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
XX Altochenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
XX Altochenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
XX Altochenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
XX Altochenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
XX Altochenko L., Wallano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
XX Altochenko L., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,
XX Altochenko S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
XX Altochenko J., Hulton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
XX Altochenko J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
XX Altochenko J., Worley A.C., Shevchenko Y., Bouffard G.G.,
XX Altochenko M. M., Sodnutz J., Myers R.M., Butterfield Y.S.,
XX Altochenko M. T., Skalska U., Smailus D.E., Schmerch A., Schein J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 160
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GO; GO:0016020; C:membrane; IEA.
GO; GO:0005164; F:tumor necrosis factor re.
GO; GO:0006955; P:immune response; IEA.
InterPro; IPR006052; TNF_family.
InterPro; IPR008983; TNF_like.
InterPro; IPR003636; TNF_subf.
Pfam; PF00229; TNF; 1.
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25-OCT-2004
25-OCT-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Prodom; PD002012; TNF subf; 1.
SMART; SM00207; TNF; 1.
PROSITE; PS00251; TNF 1; 1.
PROSITE; PS00251; TNF 2; 1.
SEQUENCE 304 AA; 34658 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata;
Actinopterygii; Neopterygii;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zgc:92320.
Name=zgc:92320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q6DHG9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q6DHG9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Whole;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brachydanio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PTLRIAAHLTGSSKRSSA-SPHNYLSYRGIGHKIHSWESSRRGHSFLYNVELWNGELVVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NLDVVESKDRVADPCWQVKWHLGKLIKKYMSRILQENMSAINGDRTQALSR--RDEPPQG
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(TrEMBLrel.
(TrEMBLrel.
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ) (Danio rerio).
; Craniata; Vertebrata; Euteleostomi;
Teleostei; Ostariophysi; Cypriniformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 809.5;
Pred. No. 3.0
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RESULT
Q7ZYX9
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Best Local S
Matches 121
[1]
SEQUENCE FROM N.A.
STRAIN=AB; TISSUB=Whole body;
STRAIN=AB; TISSUB=Whole body;
MEDLINE-22380257; PubMed=12477932; DOI=10.1073/pnas.242603899;
MEDLINE-22380257; Peimgold E.A., Grouse L.H., Derge J.G.,
Strausberg R.L., Feingold E.A., Grouse L.H., Shenmen C.M., Schuler G.D.
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T
Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.
                                                                                                                                                                                                                                                                                       Q7ZYX9
Q7ZYX9;
Q1ZYX9;
Q1_JUN_2003 (TrEMBLrel. 2
Q1_JUN_2003 (TrEMBLrel. 2
Q1_OCT_2003 (TrEMBLrel. 2
                                                                                                                                                                                     Eukaryota; Metazoa; Chordata;
Actinopterygii; Neopterygii; T
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (JUL-2004) to the EMBL/
EMBL; BC076005; AAH76005.1; -.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0005144; F:tumor necrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ProDom; PD002012; TNF subf; 1. SMART; SM00207; TNF; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jones S.J., Marra M.A.;
"Generation and initial analysis of more than 15,000
and mouse cDNA sequences.";
proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                               Tnfsf101 protein.
Name=tnfsf101;
                                                                                                                                                                                                                                                                              Infsf101
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PS50049; TNF_2; 1.
299 AA; 33526 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LILLAAILLQTIAVAVTFIYFSNVLSTMKETFSKSSVSCLMRANLRTIKGQELNGAEGKD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SYTPESEKDGAGLPNRKVYGQKIQSWESEK-GLAFLQNVELSDGELVVPQAGLYYIYSQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPCWQVKWQLRQLVRK-MILRTSEETISTVQEKQQNISPLV----RERGPQRVAAHITG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LIVIFTVLLQSLCVAVTYVYFTNELKOMODKYSKSGIACFLKED---DSYMDPNDEESMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YFR---FQEEIKENTKND------KQMVQYIY-KYTSYPDFILLMKSARNSCWSK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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Last sequence update)
Last annotation updat
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Pred. No. 3.9e-39;
7; Mismatches 82
                                                                                                                                                                                                                     ) (Danio rerio).
; Craniata; Vertebrata; Euteleostomi; Teleostei; Ostariophysi; Cypriniform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BA776793D2F11ED5 CRC64;
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                                                                                                                                                                                                                                                                                          update)
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                                                                                                                                                                                                                      Cypriniformes;
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T.E.,

SORRED DRAFT

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Query Match
Best Local :
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                                                                                090WT9;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
TNF-related apoptosis inducing ligand-like protein.
Gallus gallus (Chicken).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi.
                                                                                                                                                                                                                 Q90WT9;
Q90WT9;
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakealey R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GG; GO:0016020; C:membrane; IEA.
GO; GO:0005144; F:tumor necrosis factor
GO; GO:0006955; P:immune response; IEA.
InterPro; IPR006052; TNF family.
InterPro; IPR008983; TNF_like.
InterPro; IPR008983; TNF_subf.
Pfam; PF00229; TNF; 1.
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Jones S.J., Marra M.A.;
"Generation and initial analysis of more than 15,000 and mouse cDNA sequences.";
oron Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
  SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ProDom; PD002012; TNF subf; 1.
SMART; SM00207; TNF; 1.
PROSITE; PS50049; TNF_2; 1.
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STRAIN=AB;
                                          NCBI_TaxID=9031;
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29.2%; Pred. No. 3.
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Best Local S
Matches 93
                                                                                                                                                                 "Molecular cloning and expression of a TNF ligands in the fish ovary."; Comp. Biochem. Physiol. B, Comp. Biochem. Physiol. B, Comp. Biochem. EMBL; APS250041; AAG47640.1; -... HSSP; P50591; 1D2Q.
HSSP; P50591; 1D2Q.
ZFIN; ZDB-GENE-010801-1; tnfeff101. GO; GO:0016020; C:membrane; IEA. GO; GO:0005164; F:tumor necrosis factor re GO; GO:0005165; P:timmune response; IEA. InterPro; IPR006052; TNF_family.
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Submitted (OCT-2001) to the EMBL/GenBank/Di
EMBL; AY057941; AAL23702.1; -.

HSSP; P50591; 1D2Q.

GO; GO:0016020; C:membrane; IEA.
GO; GO:0005164; F:tumor necrosis factor re.
GO; GO:0005159; P:immune response; IEA.
Pfam; PF00229; TNF; 1.

PRINTS; PR01234; TNECROSISFCT.
PRODOM; PD002012; TNF subf; 1.

SMART; SM00207; TNF; 1.

PROSITE; PS50049; TNF2; 1.

SEQUENCE 287 AA; 32092 MW; DB06E1C9508
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Q9DDZ5;
01-MAR-2001
01-MAR-2001
01-OCT-2003
  ProDom; PD002012; TNF subf; 1.
SMART; SM00207; TNF; 1.
PROSTIE; PS50049; TNF 2; 1.
SEQUENCE 214 AA; 24093 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brachydanio rerio (Zebrafish)
Eukaryota; Metazoa; Chordata;
Actinopterygii; Neopterygii; T
Cyprinidae; Danio.
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                                                                                               InterPro; IPRO06052; TNF famil
InterPro; IPRO08983; TNF_1ike.
InterPro; IPR003636; TNF_8ubf.
Pfam; PF00229; TNF; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=7955;
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Last annotation updat
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Pred. No. 5.
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       98C002474FF691AA CRC64;
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Best Local Similarity
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05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last amotation update)
05-JUL-2004 (TrEMBLrel. 27, Last amotation update)
                                                                                           Q9ESE2; Q91Z19;
Q9ESE2; Q91Z19;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
05-JUL-2004 (Rel. 44, Last annotation update)
Tumor necrosis factor ligand superfamily member 11 (Receptor activator of nuclear factor kappa B ligand) (RANKL) (TWF-related activation-induced cytokine) (TRANCE) (Osteoprotegerin ligand) (OPGL) (Osteoclast differentiation factor) (ODF).
Name=Tnfef1; Synonyms=Opg1, Rankl, Trance;
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                    NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; C
Mammalia; Eutheria; F
 SEQUENCE FROM N.A.
TISSUE-Tibial bone;
MEDLINE-20540945; PubMed-11092398;
Xu J.K., Tan.J.K., Huang L., Gao X.H., Laird
                                                                              Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (JUN-2003) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Fragment).
Name=TNFSF10;
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                                                                 NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kere
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Lung carcinoma;
TISSUE=Lung carcinoma;
Polvi A., Ruosaari S., Vendelin J., West
Polvi A., Ruosaari S., Laitinen T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120
                                                                                                                                                                                                                                                                                                                                                                                                                              AY312579; AAR16184.1;
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                                                                                                                                                                                                                                                                                                                           39
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                                                                                                                                                                                                                                                                                                                                                    52;
                                                                                                                                                                                                                                                                                                     Н
                                                                                                                                                                                                                                                                                                                  TNELKOMODKYSKSGIACFLKEDDSYWDPNDEESMNSPCWQVKWQLRQLVRK 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RVPQDGRYYLYSQVYFRYPSPSDSDQSSVSHQLVQCIYKKTSYLNPIQLLKGVGTKCWAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QRPSAHLTLSSASDNSRPQSDMHQPQFDLHQSCRHPVHTW-ANKSFGAHLYNMTLTNGRL
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                                                                                                                                                                                                                                                                                                   TNELKOMODKYSKSGIACFLKEDDSYWDPNDEESMNSPCWQVKWQLRQLVRK
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                                                                                                                                                                                                                                                                                                                                                                                                      63
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                                                                                                                                                                                                                                                                                                                                                                                                      AA;
                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                    7638 MW;
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Primates;
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                                                                                                                                                                                                                                                                                                                                                                            19.7%;
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                                                                                                                                                                                                                                                                                                                                                  Score 291; DB; Pred. No. 1.7
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 305.5; DB 2
Pred. No. 5.3e-17;
                                                                                                                                                                                                                                                                                                                                                                                                      8F0C7936DA5AA6E6
                                                                             Craniata; Vert
Sciurognathi;
                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                   318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63
                                                                                                                                                                                                                                                                                                                                                   . 1.7e-16;
ches 0;
                                                                              Vertebrata; Euteleostomi;
thi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                            DB
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Mannila H., I
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D.,
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  Wysocki
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PSIGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACF-----LKED---PAASRFMFLALLGLGLGQVVCSIALFLYFRAQMD--PNRISEDSTRCFYRILRLRENTGL

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Query Match
Best Local S
Matches 82
                                                                 CARBOHYD
CARBOHYD
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=21662371; PubMed=11804028;
Odgren P.R., Kim N., van Wesenbeeck L., MacKay C., Mason-Savi
Odgren P.R., Expondif S.N., Lengner C., van-Hul W., Choi Y.,
Safadi F.F., Popoff S.N., Lengner C., van-Hul W., Choi Y.,
Marks S.C. Jr.;
"Evidence that the rat osteopetrotic mutation toothless (t1)
"Evidence that the rat osteopetrotic mutation toothless (t1)
"Evidence that the rat osteopetrotic mutation toothless (t1)
"Int. J. Dev. Biol. 45.853-859(2001).
"Int. J. Dev. Biol. 45.853-859(2001).
                                                                                                                                  SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF187319; AAG17031.1;
EMBL; AF425669; AAL23963.1;
HSSP; O35235; JJTZ.
RGD; 620784; Tnfsf11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Cloning, sequence and functional characterization of the rat homologue of receptor activator of NF-kB ligand."; J. Bone Miner. Res. 15:2178-2186(2000).
                                                                                                                                                                                                                               CHAIN
                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR006052; TNF family.
InterPro; IPR008983; TNF like.
InterPro; IPR003636; TNF subf.
Pfam; PF00229; TNF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (Some send an email to license@isb-sib.ch).
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SEQUENCE OF 266-318 FROM N.A.
                                                                                                                                                  DOMAIN
                                                                                                                                                                                 TRANSMEM
                                                                                                                                                                                                                                                                                                              ProDom; PD002012; TNF subf; 1.
SMART; SM00207; TNF 1; FALSE_NEG.
PROSITE; PS00251; TNF 1; FALSE_NEG.
PROSITE; PS50049; TNF_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-Fischer 344;
                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zheng M.H.;
                                                                                                                                                                                                                                                                                               Cytokine;
                                                                                                                                                                                                                                                                               Tansmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: Cytokine that binds to TNFRSF11B/OPG and to FUNCTION: Cytokine that binds to TNFRSF11B/OPG and activation factor TNFRSF11A/RANK. Osteoclast differentiation and activation factor Augments the ability of dendritic cells to stimulate naive T-ce proliferation. May be an important regulator of interactions between T cells and dendritic cells and may play a role in the regulation of the T cell-dependent immune response. May also plan important role in enhanced bone-resorption in humoral hypercalcemia of malignancy.
SUBCULIULAR LOCATION: Type II membrane protein and secreted (By SUBCULIULAR LOCATION: Type II membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE SPECIFICITY: Highly expressed in thymus and bone PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity).
SIMILARITY: Belongs to the tumor necrosis factor family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     similarity)
     82;
                    Similarity
                                                                                                                                                                                                                                                                                               Differentiation; Glycoprotein; Receptor; Signal-anchor;
                                                                   318
     Conservative
                                                                                                                69
140
199
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                                                                    A,
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141
199
264
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                                                                    35370
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68
                  18.1%;
                                                                    ¥;
     55;
                                                                 protein (Potential).
Extracellular (Potential).
Cleavage (By similarity).
N-linked (GlcNAc. . .) (Potential).
N-linked (GlcNAc. . .) (Potential).
I -> M (in Ref. 2).
I -> M (in Ref. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . .
Pred. No. 1.2e
5; Mismatches
                                   Score 267.5;
                                                                                                                                                                              Cytoplasmic (Potential).
Signal-anchor for type II membrane
                                                                                                                                                                                                                Tumor necrosis factor ligand member 11, soluble form.
                                                                                                                                                                                                                                                               Tumor necrosis factor ligand
                                                                                                                                                                                                                                                 11, membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        noved. Usage by and for commercial
(See http://www.isb-sib.ch/announce/
                     1.2e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         There are no restrictions on the mg as its content is in no we red. Usage have
                                    BB
   106;
                                   1;
                                                                                                                                                                                                                                                 form
                                   Length
     Indels
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Thoi Y.,
                                      318;
                                                                                                                                                                                                                               superfamily
                                                                                                                                                                                                                                                               superfamily
     57;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tissues.
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     Gaps
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RESULT TRESULT TO THE PROPERTY OF THE PROPERTY
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SEQUENCE FROM N.A. (ISOroxu, .,
SEQUENCE FROM N.A. (ISOroxu, .,
TISSUE=Thymic lymphoma;
MEDLINE=98032977; PubMed=9367155; DOI=10.1038/36593;
MEDLINE=98032977; PubMed=9367155; DOI=10.1038/36593;
MEDLINE=98032977; PubMed=9367155; DOI=10.1038/36593;
MEDLINE=98032977; PubMed=980715; DOI=10.1038/36593;
MEDLINE=98032977; PubMed=980715; DOI=10.1038/36593;
MEDLINE=98032977; PubMed=980715; DOI=10.1038/36593;
MEDLINE=98032977; PubMed=9367155; DOI=10.1038/36593;
MEDLINE=98032977; PubMed=98032977;
MEDLINE=98032977; PubMed=9803297;
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035235; 035336; Q9JUK8; Q9JUK9; Q9RIY0;

16-OCT-2001 (Rel. 40, Created)

16-OCT-2004 (Rel. 40, Last sequence update)

25-OCT-2004 (Rel. 45, Last annotation update)

25-OCT-2004 (Rel. 45, Last annotation update)

70-mor necrosis factor ligand superfamily member 11 (Receptor activator of nuclear factor Lagand superfamily member 11 (Receptor activator of nuclear factor Kappa B ligand) (RANKL) (TNP-related activation-induced cytokine) (TRANCE) (Osteoprotegorin ligand) (OpGi) (Osteoplast Linduced cytokine) (TRANCE) (Osteoprotegorin ligand) (OpGi) (Osteoplast Linduced cytokine) (TRANCE) (Osteoprotegorin ligand) (OpGi) (Osteoplast Linduced cytokine) (TRANCE) (Osteoprotegorin ligand)
                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-9827661; PubMed-9568710; DOI=10.1016/S0092-86 Lacey D.L. Timms E., Tan H.-L., Kelley M.J., Dunstan Burgess T., Elliott R., Colombero A., Elliott G., Scul Sullivan J., Hawkins N., Davy E., Capparelli C., Eli F. Kaufman S., Sarosi I., Shalhoub V., Senaldi G., Guo J.
                                                                                                                                                                                                                     differentiation and a Cell 93:165-176 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=97460112; PubMed=9312132; DOI=
Wong B.R., Rho J., Arron J., Robinson
Kalachikov S., Cayani E., Bartlett F.S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           differentiation
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                               MEDLINE=98188248; PubMed=9520411; Yasuda H., Shima N., Nakagawa N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=Tnfsf11;
                                                                                                                                                                                                                                                                                               "Osteoprotegerin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              homologue of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nomologue of the TNF receptor dendritic-cell function.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                390:175-179(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 is a novel ligand of the tumor tivates c-Jun N-terminal kinase . Chem. 272:25190-25194(1997).
                                                                                                                                               FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QDSTLESEDTEALPDSCRRMKQAFQ-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   marrow;
                                                                                                            marrow stroma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synonyms=OPGL,
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                                                                                                                                                                                                                                                                                               ligand is a cytokine that regulates
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                                                                                                                                               (ISOFORM 1).
                                                                                                                                                                                                                                                                activation
Α.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vert
Sciurognathi;
   Yano
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Osteoclastogenesis-inhibitory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and
DOI=10.1073/pnas.95.7.3597;
Yamaguchi K., Kinosaki M.,
o K., Goto M., Murakami A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOI=10.1074/jbc.272.40.25190
nson E., Orlinick J., Chao M.,
t F.S. III, Frankel W.N., Lee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOI=10.1016/S0092-8674(00)81569-X;
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in T cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vertebrata; Euteleostomi;
thi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ligand
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                                                                                                                                                                                                                                                                                                                                                                     Scully S., Hsu H., Eli A., Qian Y.-X., no J., Delaney J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cosman D.,
                                                                                                                                                                                                                                                                                                   osteoclast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   factor)
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2.2-A res
J. Biol.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 139-147, PROCESSING, AND N-GLYCOSYLATION.
MEDLINE=99240759; PubMed=10224132; DOI=10.1074/jbc.274.19.13613;
MEDLINE=99240759; PubMed=10224132; DOI=10.1074/jbc.274.19.13613;
Lum L., Wong B.R., Josien R., Becherer J.D., Erdjument-Bromage H.,
Schloendorff J., Tempst P., Choi Y., Blobel C.P.;
Schloendorff J., Tempst P., Choi Y., Blobel C.P.;
"Evidence for a role of a tumor necrosis factor-alpha (TNF-alpha)-
"Evidence for a role of a tumor necrosis factor-alpha (TNF-alpha)-
"Converting enzyme-like processe in shedding of TRANCE, a TNF family
member involved in osteoclastogenesis and dendritic cell survival.
J., Biol. Chem. 274:13613-13618(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORMS 1, 2 AND 3).
MEDLINE=21150053; PubMed=11250921; DOI=10.1210/en.142.4.1419;
Ikeda T., Kasai M., Utsuyama M., Hirokawa K.;
"Determination of three isoforms of the receptor activator of factor-kappaB ligand and their differential expression in bor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Cloning and characterization differentiation factor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lam J., Nelson C.A., Ross F.P., Teitelk
"Crystal structure of the TRANCE/RANKL
of receptor-ligand specificity."
J. Clin. Invest. 108:971-979(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS)
MEDLINE=21464816; PubMed=11581298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Endocrinology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kodaira K., Kodaira
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Crystal structure of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=21839021;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=99214075;
PTM: N-glycosylated.

PTM: The soluble form of isoform 1 derives from the membrane by proteolytic processing. The cleavage may be catalyzed by ADAM17. A further shorter soluble form was observed.

DISEASE: Deficiency in Tnfsfil results in failure to form lob
                                                                                                                                                                                                                                                                  hypercalcemia of malignancy.
SUBUNIT: Homotriner.
SUBCELLULAR LOCATION: Type II me
(1soforms 1 and 2); Cytoplasmic
ALTERNATIVE PRODUCTS:
                                                                                                                   TISSUE SPECIFICITY:
but not in nonlympho
                                                                                                                                                                                                                                                                                                                                                      proliferation. May be an important regulator of interactions between T cells and dendritic cells and may play a role in the regulation of the T cell-dependent immune response. May also an important role in enhanced bone-resorption in humoral
                                                                                                                                                                                                                                                                                                                                                                                                                       3iol. Chem. 277:6631-6636(2002).
FUNCTION: Cytokine that binds to TNFRSF11B/OPG and to TNFRSF11B/RANK. Obteoclast differentiation and activation fungments the ability of dendritic cells to stimulate naive
                                                                                   the trabecular bone and
                                                                                                       cells
                                                                                                                                                                                                                                                      Event=Alternative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           resolution.";
                                                                                                                                                      IBoId=035235-3; Sequence=VSP_006448;
                                                                                                                                                                                       IsoId=035235-2;
                                                                                                                                                                                                                     IsoId=035235-1; Sequence=Displayed;
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                                                                                                     but not in
                                                                                                 SPECIFICITY: Highly expressed in thymus and in nonlymphoid tissues and is abundantly e ut not in B cells. A high level expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N.A.
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PubMed=11733492; DOI=10.1074/jbc.M106525200;

hi K., Ubukata O., Hayashi S., Okada F., Hata T.;

e of the extracellular domain of mouse RANK ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=10196481;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ISOFORM
                                                                                                                                                                                    Sequence=VSP_006449;
                                                                                                                                                                                                                                                    splicing; Named isoforms=3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Teitelbaum
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                                                                                                                                                                                                                                                                                                       membrane
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Yasuda
                                                                                                                   ressed in thymus and lymph nodes and is abundantly expressed in
                                                                                                                                                                                                                                                                                     (isoform 3).
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cytokine m
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H., Shima N., Murakami A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     encoding
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form lobulo

alveolar mammary structures during pregnancy, resulting in death of newborns. Trance-deficient mice show severe osteopetrosis, with no osteoclasts, marrow spaces, or tooth eruption, and exhibit profound growth retardation at several skeletal sites, including the limbs, skull, and vertebrae and have marked chondrodysplasia, with thick, irregular growth plates and a relative increase in hypertrophic chondrocytes.

SIMILARITY: Belongs to the tumor necrosis factor family.

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RMBL; AF013170; AAC71061.1; -...

REMBL; AF019048; AAB86812.1; -...

REMBL; AF053713; AAC4013.1; -...

REMBL; AF053713; AAC4013.1; -...

REMBL; AB008426; BAA25625.1; -...

REMBL; AB022039; BAA36970.1; JOINED.

REMBL; AB022038; BAA36970.1; JOINED.

REMBL; AB022038; BAA36970.1; JOINED.

REMBL; AB022038; BAA36970.1; JOINED.

REMBL; AB022071; BAA97259.1; -...

REMBL; AB032772; BAA97259.1; -...

REMBL; AB032772; BAA97259.1; -...

REMBL; AB036798; F:protein binding; IPI.

REMBL; AB036798; F:protein binding; IPI.

ROG; GO:0045813; P:protein binding; IPI.

ROG; GO:004583; P:protein binding; IDA.

ROG; GO:004587; P:regulation of osteoclast differentiation; IDA.

ROG; GO:0045670; P:regulation; IDA.

ROG; GO:0045670; P:regulation; IDA.

ROG; GO:0045670; P:regulation of osteoclast differentiation; IDA.

ROG; GO:0045670; P:regulation; IDA.

ROG; 
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ProDom; PD002012; TNF_subf; 1.
SMART; SM00207; TNF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00251; TNF_1; FALSE_NEG PROSITE; PS50049; TNF_2; 1.
                                                                                                                                                                                                                      VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                  TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3D-structure; Alternative splicing; Cytokine; Differentiation;
Direct protein sequencing; Glycoprotein; Receptor; Signal-anchor;
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69
                                                                                                                                        isoform 2).
/FTId=VSP_006449.
G -> D (in Ref. 2).
Missing (in Ref. 5).
                                                                                                                                                                                                                                                                                                                                                                        member 11, soluble form.
Cytoplasmic (Potential).
Signal-anchor for type II membrane
                                                                                                                                                                                                                                        N-linked (GlcNAc...)
N-linked (GlcNAc...)
Missing (in isoform 3)
/FTId=VSP_006448.
                                                                                                                                                                                                                                                                                                                     Cleavage.
                                                                                                                                                                                                                                                                                                                                         protein (Potential).
Extracellular (Potential).
                                                                                                                                                                                                                      SSEEMGSGPGVPHEGPLHPAPSAPAPAPPPA ->
                                                                                                                                                                                                                                                                                                                                                                                                                                          Tumor necrosis factor ligand superfamily
                                                                                                                                                                                                                                                                                                                                                                                                                                                               member 11, membrane form.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tumor necrosis factor ligand
                                                                                                                                                                                                                                                                                  (Potential)
(Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               superfamily
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RESULT
TN11_HU
ALD DE REPRESENTATION DE LA PRESENTATION DE LA PRES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TN11 HUMAN STANDARD; PRT; 317 AA.

014788; 014723; Q96Q17; Q992Q3;

16-OCT-2001 (Rel. 40, Created)

16-OCT-2001 (Rel. 44, Last sequence update)

17-007 necrosis factor ligand superfamily member 11 (Receptor activator of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-induced cytokine) (TRANCE) (Osteoprotegerin ligand) (OPGL) (Osteoclast differentiation factor) (ODF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LT 12
HUMAN
                                                                                                 [3] SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3). Ikeda T., Kuroyama H., Hirokawa K.; Ikeda T., Kuroyama H., Hirokawa K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Bone marrow, and Peripheral blood;
MEDLINE-98039977; PubMed-9367155; DOI=10.1038/36593;
Anderson D.M., Maraskovsky E., Billingsley W.L., Doug
Tometsko M.E., Roux E.R., Teepe M.C., DuBose R.F., C
Galibert L.;
                                                                                                                                                                                                               "Osteoprotegerin ligand is a cy differentiation and activation. Cell 93:165-176(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                            Lacey D.L., Timms B., Tan H.-L., Kelley M.J., Dunstan C.R., Burgess T., Elliott R., Colombero A., Elliott G., Scully S., Hsu Sullivan J., Hawkins N., Davy B., Capparelli C., Eli A., Olan Y.-Kaufman S., Sarosi I., Shalhoub V., Senaldi G., Guo J., Delaney J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=TNFSF11; Synonyms=OPGL, RANKL, Homo sapiens (Human)
                         SEQUENCE OF 73-317
                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Lymph node;
MEDLINE=98227661;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "A homologue of the TNF receptor and dendritic-cell function.";
TISSUE=Thymocytes;
                                                                                "Determination of hur
Submitted (JUN-2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       dendritic-cell functi
ure 390:175-179(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKV 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMVYVVKTSIKIPSSHNLMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYT-SYPDPILLMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----VRERGPORVA--AHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QDSTLESEDTLPDSCRRMKQAFQGAVQK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WDP--NDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACF----LKEDDSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EGSWLDVAQRGKPEAQPFAHLT-----INAASIPSGSHKVTL----SSWYHDR-GWAKIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PAASRSMFLALLGLGLGQVVCSIALFLYFRAQMD--PNRISEDSTHCFYRILRLHENAGL 100
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                                                                                human
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                            FROM
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                            N.A
                                                                                RANKL
the EM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ۳.
                                                                                   EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                    cytokine
on.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 258.5; DB 1
Pred. No. 6.3e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and its ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                               DOI=10.1016/S0092-8674 (00) 81569-X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANCE;
                                                                                                                                                                                                                                                                              that
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                                                                                                                                                                                                                                                                              regulates
                                                                                      databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             enhance T-cell growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dougall W.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cosman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            316;
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EMBL; AF019047; AAB86811.1; --
EMBL; AF053712; AAC39731.1; --
EMBL; AB064269; BAB79694.1; --
EMBL; AB061227; BAB71768.1; --
EMBL; AB064270; BAB79695.1; --
EMBL; AB0613171; AAC51762.1; --
EMBL; AB037599; BAA90488.1; --
                              Genew; HGNC:11926; TNFSF11.

MIM; 602642; ...

GO; GO:0005576; C:extracellular; NAS.

GO; GO:0005887; C:integral to plasma membrane; NAS.

GO; GO:0005164; F:tumor necrosis factor receptor binding;

GO; GO:0006955; F:immune response; NAS.

GO; GO:0030316; P:osteoclast differentiation; NAS.

InterPro; IPR006052; TNF family.

InterPro; IPR008983; TNF_like.

InterPro; IPR003636; TNF_subf.
                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Elthe European Bioinformatics Institute. There are no restuse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biochem. Biophys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nagai M., Kyakumoto S., Sato N.; "Cancer cells responsible for humoral hypercalcemia encoding a secreted form of ODF/TRANCE that induces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=97460112; PubMed=9312132; DOI=10.1074/jbc.272.40.25190; Wong B.R., Rho J., Arron J., Robinson E., Orlinick J., Chao M., Kalachikov S., Cayani E., Bartlett F.S. III, Frankel W.N., Lee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=20175237; PubMed=10708588; DOI=10.1006/bbrc.2000.2314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          formation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "TRANCE is a novel ligand of the tumor nec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <u>5</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE SPECIFICATE INTEGRAL BOOK Leukocytes, bone marrow, nearc, spleen, peripheral blood Leukocytes, bone marrow, nearc, skeletal muscle, stomach and thyroid.

INDUCTION: Up-regulated by T cell receptor stimulation. INDUCTION: The soluble form of isoform 1 derives from the memb PTM: The soluble form of isoform 1 derives from the memb PTM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         by proteolytic processing (By similarity). The cleavage catalyzed by ADAM17.
SIMILARITY: Belongs to the tumor necrosis factor family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=3;
IsoId=Ol4788-3; Sequence=VSP_006446;
TISSUE SPECIFICITY: Highest in the peripheral lymph nodes, weak in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypercalcemia of malignancy.
SUBUNIT: Homotrimer (By similarity).
SUBCELLULAR LOCATION: Type II membrane protein (isoforms SUBCELLULAR LOCATION: Type II membrane protein (isoform 2). A soluble form of isoform 1 arises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chem. Blophys. Res. Commun. 269:532-536(2000).

FUNCTION: Cytckine that binds to TMPRSF11B/OPG and to TWPRSF11B/OPG and to Stimulate naive T-cell Augments the ability of dendritic cells to stimulate naive T-cell proliferation. May be an important regulator of interactions between T cells and dendritic cells and may play a role in the regulation of the T cell-dependent immune response. May also play an important role in enhanced bone-resorption in humoral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          proteolytic processing (By similarity). ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Event=Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IsoId=014788-1; Sequence=Displayed;
ime=2; Synonyms=SODF;
IsoId=014788-2; Sequence=VSP_006447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                272:25190-25194 (1997).
                      TNF;
TNF_subf; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence=VSP_006447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       splicing; Named isoforms=3;
                                                                                                                                                                                                                                                                                                                                                                                                                                      (See http://www.isb-sib
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       necrosis factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             osteoclast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             express mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lee S.Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          FO.
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01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Timor necrosis factor ligand superfamily me
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SEQUENCE
                                        Suda T., Nagata S.; "Generalized lymphoproliferative mutation in the Fas ligand.";
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CARBOHYD
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SITE
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PROSITE; PS00251; TNF]; 1.
PROSITE; PS50049; TNF_2; 1.
Alternative splicing; Cycokine; Differentiation; Glycoprotein;
Receptor; Signal-anchor; Transmembrane.
                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                  Name=Tnfsf6; Synonyms=APT1LG1, Fas1, Mus musculus (Mouse).
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                                                                         Takahashi
                                                                                   MEDLINE=94185175; PubMed=7511063;
                                                                                             SEQUENCE FROM N.A.
          SEQUENCE FROM N.A.
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                                76:969-976(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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Pred. No. 2.4e-12;
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N-linked (GlcNAc. ..)
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                                                                         C.I.,
                                                    disease
                                                                        DOI=10.1016/0092-8674(94)90375-1;
C.I., Jenkins N.A., Copeland N.G.,
           AND
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           3D-STRUCTURE
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MEDLINE-95196085; PubMede-7889405; DOI=10.1016/1074-7613(94)90106-6;
Lynch D.H., Watson M.L., Alderson M.R., Baum P.R., Miller R.E.,
Tough T., Gibson M., Davis-Smith T., Smith C.A., Hunter K.;
"The mouse Fas-ligand gene is mutated in gld mice and is part of a 7 family gene cluster.";
                                                  This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHARACTERIZATION OF VARIANT GLD.
MEDLINE=96091792; PubMeds7495745;
Hahne M., Peitsch M.C., Irmler M., Schro
Rousseau M., Bron C., Renno T., French I
"Characterization of the non-functional
Int. Immunol. 7:1381-1386(1995).
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[3]
SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino
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"Mus musculus Balb/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=BALB/c
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STRAIN=BALB/c,
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Kayagaki N., Yamaguchi N., Nagao F., Matsuo S., Maeda H., Oku
                              between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Polymorphism of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Emmunity
                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that transduces the apoptotic signal into cells. May be involved in cytotoxic T cell mediated apoptosis and in T cell development. TNFRSF6/FAS-mediated apoptosis may have a role in the induction of peripheral tolerance, in the antigen-stimulated suicide of mature T cells, or both. Binding to the decoy receptor TNFRSF6B/DcR3 modulates its effects (By similarity). SUBCELIULAR LOCATION: Type II membrane protein (isoform FASI);
                                                                                                                   IsoId-P41047-2; Sequence=VSP 006445; PTM: The soluble form derives from the membrane proteolytic processing (By similarity). DISEASE: A deficiency in this protein is the cau lymphoproliferation disease phenotype (gld). Gld lymphadenopathy and autoantibody production. The recessively inherited.
                                                                                             SIMILARITY: Belongs to the tumor necrosis factor family.
                                                                                                                                                                                                                                                                                                                                                                                           Secreted (isoforms FASL and ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                     Event=Alternative
SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
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ALB/c, C3H, (
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s ligand differs from
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EMBL; U10984; AAA19778.1; -.
EMBL; S76752; AAB33780.1; -.
EMBL; U58995; AAB02915.1; -.
EMBL; AF119335; AAD52106.1; -.
EMBL; AF33662; A53362.
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PRINTS; PR01234; TNECROSISFCT.
PRODOM; PD002012; TNF_subf; 1.
PROSITE; PS00251; TNF_1; 1.
PROSITE; PS0049; TNF_2; 1.
PROSITE; PS50049; TNF_2; 1.
Alternative splicing; Apoptosis; Cytokine; Glycoprotein; Polymorphism; Signal-anchor; Glycoprotein; Polymorphism; Signal-anchor;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHAIN
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                                                                                                                                                                                                                                                                                   VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam;
                                                                                                                                                                                                                                                                                                         VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PF00229; TNF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P50591; 1DG6
                                                                                                                                                   83
                                                                                                                                                                         51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; IPRO08064; Fas_ligand.
; IPRO06053; TNF_abc.
; IPRO06053; TNF_family.
; IPR008983; TNF_like.
; IPR003636; TNF_subf.
                                                                                                     NEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKN
                                                                                                                         ELREFTNOSL-----KVSSFEKQIANPSTPSEKKEPRSV
                                                                                                                                                  QLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSK
                                                            DKQMVQYIY-KYTSYPDPILLMKSAR-NSCWSKDAEYGLYSIYQGGIFELKENDRIFVSV
SQLSLINFEESKTFFGLY
                    TNEHLIDMDHEASFFGAF
                                         NQPLNHKVYMRNSKYPEDLVLMEEKRLNYCTT--GQIWAHSSYLGAVFNLTSADHLYVNI
                                                                                   SIPL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   on-profit institutions as long not this statement is not removed. equires a license agreement (See email to license@isb-sib.ch).
                                                                                                                                                                                                                    279
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79
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                                                                                   -EWEDT-YGTALISGVKYKKGGLVINETGLYFVYSKVYFRGQ
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51
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100
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                                                                                                                                                                                  12.8%;
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;
                                                                                                                                                                         50;
                     278
                                                                                                                                                                                                                                                                                                                                                                                                                        Cytoplasmic (Potential).
Signal-anchor for
                                                                                                                                                                                                                                                                                  Missing (in /FTId=VSP A (in
                                                                                                                                                                                                                                                                                                                  N-linked
N-linked
N-linked
                                                                                                                                                                                                                                     T -> A (in strain BALB/c, strain DBA/1 and strain DBA/2; enhances cytotoxicity by G (in strain BALB/c, strain DBA/1 and strain DBA/2; enhances cytotoxicity by C (in gld; abolishes binding of E -> L (in gld; abolishes binding of E
                                                                                                                                                                                                                                                                                                                                                                       Poly-Pro.
Cleavage
                                                                                                                                                                         Pred. No. 2.50
); Mismatches
                                                                                                                                                                                    Score 189.5;
Pred. No. 2.
                                                                                                                                                                                                                               to its receptor)
                                                                                                                                                                                                                                                                                                                                                                                             Pro-rich.
                                                                                                                                                                                                                                                                                                                                                                                                       Signal-anchor for type II protein (Potential). Extracellular (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tumor necrosis factor ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        member 6, membrane
                                                                                                                                                                                                                                                                                                                                                             Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tumor necrosis factor ligand
                                                                                                                                                                                                                     37972E2728E0A1CA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cytokine; Disease mutation;
                                                                                                                                                                                                                                                                                                   d (GlcNAc. ..) (Poten d) (GlcNAc. ..) (Poten d) (GlcNAc. ..) (Poten d) (GlcNAc. ..) (Poten d) (In isoform FasLS)
                                                                                                                                                                                                                                                                                                                                                                     (Ву
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                                                                                                                                                                                     .5e-07;
                                                                                                                                                                                                                                                                                                                                                                        similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . Usage by and for http://www.isb-sib.
                                                                                                                                                                                              DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transmembrane
                                                                                                                                                                         64;
                                                                                                                                                                          Indels
                                                                                                                                                                                            Length
                                                                                                                                AHLTG
                                                                                                                                                                                                                                                                                                                  (Potential).
(Potential).
(Potential).
(Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                               membrane
                                                                                                                                                                                                                                          cytotoxicity).
binding of FASL
                                                                                                                                                                                                                                                                         cytotoxicity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              superfamily
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                                                                                                                                                                         33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .ch/announce,
                                                                                                                                                                         Gaps
                                                                                     SCN
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                                           259
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RESULT 14
   EMBL; AF344847; AAK37606.1; -.
HSSB; P50591; 1D2Q.
InterPro; IPR008064; Fas_ligand.
InterPro; IPR008053; TNF_abc.
InterPro; IPR006053; TNF_family.
InterPro; IPR006052; TNF_family.
InterPro; IPR00893; TNF_like.
InterPro; IPR003636; TNF_subf.
Pfam; PF00229; TNF; 1.
PFANTS; PR01601; FASLIGANO.
PRINTS; PR01234; TNECROSISFCT.
PRODOM; PD002012; TNF subf; 1.
SMART; SM00207; TNF; I.
PROGITE; PS00251; TNF; 1.
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               DOMAIN
DOMAIN
DOMAIN
SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Lymphocytes;
MEDLINE-21383618; PubMed=11491535; DOI=10.1007/8002510100322;
Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
Weiss W.R., Ansari A.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CD95L protein)
Name=TNFSF6; Synonyms=CD95L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation updat
Tumor necrosis factor ligand superfamily me
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 DISULFIC
                                                                                                                    DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Cloning, sequencing, and homology analysis of nonhuman primate Fas/Fas-ligand and co-stimulatory molecules."; Immunogenetics 53:315-328(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cercopithecinae; Cercocebus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cercocebus torquatus atys (Red-crowned mangabey) (Sooty mangabey)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-FEB-2003
                                                                                                  TRANSMEM
                                                                                                                                                                                                                  PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that transduces the apoptotic signal into cells. May be involved in cytotoxic T cell mediated apoptosis and in T cell development. TNFRSF6/FAS-mediated apoptosis may have a role in the induction of peripheral tolerance, in the antigen-stimulated suicide of mature T cells, or both. Binding to the decoy receptor TNFRSF6B/DcR3 modulates its effects (By similarity).

SUBCELLULAR LOCATION: Type II membrane protein and secreted (By SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way incompared the content is not as long as its content is in no way.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity). SIMILARITY: Belongs to the tumor necrosis factor family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CERTO
                                                                                                                                                                 PS50049; TNF_2; 1.

B; Cytokine; Glycoprotein; Signal-anchor; Transmembrane.

B; Cytokine; Glycoprotein; Signal-anchor; Transmembrane.

Tumor necrosis factor ligand superf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Rel. 41,
(Rel. 41,
(Rel. 44,
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                                                                                                                                                                                                                   TNF_1; 1.
TNF_2; 1.
 280
69
64
129
232
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                                                                                                                    90
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Poly-Pro.
Cleavage (By
Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nnotation update) superfamily member
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FASL;
                                                                                             Cytoplasmic (Potential).
Signal-anchor for type II membrane
                                                                                                                                Tumor necrosis factor ligand member 6, soluble form (By s:
                                                                protein (Potent:
Extracellular (1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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RESULT 15
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                    TNP6 HUMAN STANDARD; PRT; 281 AA. P40023; Q9BZP9; O1-FEB-1996 (Rel. 33, Created) O1-FEB-1996 (Rel. 33, Last sequence update) O5-JUL-2004 (Rel. 44, Last annotation update) Tumor necrosis factor ligand superfamily member (Apoptosis antigen ligand) (APTL) (CD178 antigen Name=TNFSP6; Synonyms=APTLIG1, FASL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
CARBOHYD
CARBOHYD
SEQUENCE
                                                  Mita E., Hayashi N., Iio S., Fusamoto H., Kamada T., "Role of Fas ligand in apopto"
                                                                                      SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=95071350; PubMed=7980502;
                                                                                                                                                                    Int. Immunol.
                                                                                                                                                                                                                                                                                                                                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TISSUE≃Leukocyte;
         SEQUENCE FROM N.A.
                                 Biochem.
                                                                         Mita E.,
                                                                                                                        Submitted
                                                                                                                                    Schaetzlein
                                                                                                                                             SEQUENCE
                                                                                                                                                                                      Takahashi T., Tanaka M., Inazawa J
"Human Fas ligand: gene structure,
                                                                                                                                                                                                                MEDLINE=95127560;
                                                                                                                                                                                                                            SEQUENCE FROM
                                                                                                                                                                                                                                                                      "Fas ligand mediates activation-induced
                                                                                                                                                                                                                                                                                             MEDLINE=95105731;
                                                                                                                                                                                                                                                                                                        SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human)
                                                                                                                                                                                                                                                lymphocytes."
J. Exp. Med.
                                                                                                                                                                                                                                                                                   Alderson M.
                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                    FROM
ein C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IYSQTYFRFQEEIKENTKNDKQMVQYIY-KYTSYPDPILLMKSARNSCWSKDAEYGLYSI
                               Biophys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YQGGIFELKENDRIFYSYTNEHLIDMDHEASFFGAF 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AHLTG------KPNSRSMPL-----EWEDT-YGIVLLSGVKYKKGGLVINETGLYF
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                                                                                                                      FROM N.A. (ISOFORM in C.E., Poehlmann (JUN-1995) to the
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nilarity 22.1%;
Conservative 5
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                                                                                                                                                                                                    560; PubMed=7826947;
Tanaka M., Inazawa J.,
                                                                                                                                                                     6:1567-1574(1994)
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249
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31407
                                 Res. Commun.
                                                                                                                                                                                                                                                                                              . (ISOFORM 1).
PubMed=7528780;
           (ISOFORM
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                                                     apoptosis
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                                                                                                                       R., Philippsen P., EMBL/GenBank/DDBJ
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Pred. No. 4e-0
56; Mismatches
                                                                            Takehara
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N-linked (GlcNAc...)
N-linked (GlcNAc...)
N-29EA60067B7D398 CRC
                                 204:468-474(1994)
                                                      induced
                                                                                                                                                                                                                                                                                                                                                                                     (CD178 antigen).
                                                                                                                                                                                          chromosomal location and spec
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                                                                            Hijioka
                                                      hepatitis
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                                                                                                                                    Eibel H.;
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                                                                            Kasahara
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RA Strausberg R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K., Ra Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Villalon D.K., Mala S., Garcia A.M., Gay L.J., Hulyk S.W., RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schein J.E., Jones S.J.M., Marra M.A., Smailus D.B., RA Rodriguez C.N., Krzywinski M.I., Skalska U., Smailus D.B., RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., French C. Matl. Arad. Sch'i U.S. a Gallegolia C. C., Natl. Arad. Sch'i U.S. a Gallegolia C. C., She'i U.S. a Gallegolia C. C., Natl. Arad. Sch'i U.S. a Gallegolia C. C., Natl. Arad. Sch'i U.S. a Gallegolia C. C., She'i U.S. a Gallegolia C. C., Natl. Arad. Sch'i U.S. a Gallegolia C. C.,
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Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=97373583; PubMed=9228058; DOI=10.1074/jbc.272.30.18827; Schneider P., Bodmer J.-L., Holler N., Mattmann C., Scuderi P., Terskikh A., Peitsch M.C., Tschopp J., "Characterization of Fas (Apo-1, CD95)-Fas ligand interaction."; Biol. Chem. 272:18827-18833(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=98087475; PubMed=9427603;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHARACTERIZATION,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Blood;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=22388257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM
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PIM: 1116 proteosylic processing.
proteolytic processing.
DISEASE: Defects in TNFSP6 are a cause of autoimmune
DISEASE: Defects in TNFSP6 are a cause of autoimmune
lymphoproliferative syndrome (ALPS) [MIM:601859]; also known
lymphoproliferative syndrome (CSS). ALPS is a childhood syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Type II membrane into the extracellular fluid, probably
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that transduces the apoptotic signal into cells. May be involved in cytotoxic T cell mediated apoptosis and in T cell development. TNFRSF6/FAS-mediated apoptosis may have a role in the induction of peripheral tolerance, in the antigen-stimulated suicide of mature T cells, or both. Binding to the decoy receptor TNFRSF6B/DcR3
                                                                                                                                                                                                      PTM: N-glycosylated.
PTM: The soluble form derives
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBUNIT: Homotrimer (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            modulates its effects.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Event=Alternative
                                                                                                                                                                                                                                                                                          IsoId=P48023-2;
                                                                                                                                                                                                                                                                                                                                                                 IsoId=P48023-1;
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tion and characterization of a new naturally occuring variant
Fas ligand that is expressed only in membrane bound form.";
ted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   M., Nakanishi Y.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Adachi M., Nagata
                                                                                                                                                                                                                                                                              Sequence=VSP_006443,
                                                                                                                                                                                                                                                                                                                                                             Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                     splicing; Named isoforms=2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OF PRO-206; TYR-218 AND PHE-2
DOI=10.1074/jbc.272.30.18827;
r N., Mattmann C., Scuderi P.,
                                                                                                                                                                                                          from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein. May be released
by cleavage form the cel
                                                                                                                                                                                                          membrane form
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EMBL; U08137; AAC50071.1; -.
EMBL; U11821; AAC50124.1; -.
EMBL; D38122; BAA07320.1; -.
EMBL; AF288573; AAG60017.1; -.
EMBL; 296050; CAB09424.1; -.
EMBL; BC017502; AAH17502.1; -.
EMBL; AR013303; BAA32542.1; -.
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HSSP; P50591; 1D2Q.
Genew; HGNC:11936; TNF
H-InvDB; HIXO001337;
MIM; 134638; -...
MIM; 601859; -...
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CARBOHYD
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GO; GO:0005102; F:receptor binding; TAS.
GO; GO:0007267; P:cell-cell signaling; TAS.
GO; GO:0007267; P:cell-cell signaling; TAS.
GO; GO:0006917; P:induction of apoptosis; TAS.
GO; GO:0007165; P:signal transduction of I-kappaB kinase/NF-k.
GO; GO:0007165; P:signal transduction; TAS.
InterPro; IPR008064; Fas ligand.
InterPro; IPR008063; TNF_abc.
InterPro; IPR006053; TNF_abc.
InterPro; IPR006053; TNF_sbc.
InterPro; IPR006053; TNF_sbc.
InterPro; IPR003656; TNF_subf.
Pfam; PF00229; TNF]; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                             CHAIN
                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR01681; FASLIGAND.
PRINTS; PR01234; TNECROSISFCT.
PRODOM; PD002012; TNF subf; 1.
PROSITE; PS00251; TNF 1; 1.
PROSITE; PS50049; TNF 2; 1.
Alternative splicing; Antigen; Apoptosis; Cytokine;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               involving hemolytic anemia and thrombocytopenia with massive lymphadenopathy and splenomegaly.

SIMILARITY: Belongs to the tumor necrosis factor family.

DATABASE: NAME=PROW; NOTE=PROW 2:59-69(2001);

WWW-"http://www.ncbi.nlm.nih.gov/prow/guide/333879674_g.htm"
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102
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                                           Missing (In isoform Z).

Missing (In isoform Z).

/FTId=VSP_006444.

P->D,F,R: Lowers binding to TNFRSF6
P->D,F,R: Toward binding to TNFRSF6
P->D,F,R: Toward binding to TNFRSF6
                                                                                                                                                                                                                                                                                 Tumor necrosis factor 1: member 6, soluble form. Cytoplasmic (Potential)
           abolishes cytotoxity F->L: Abolishes bind
                                reduces cytotoxity more than 100-fold Y->F,R: Lowers binding to TNFRSF6 and
                                                                                                                                  STSQMHTASSL ->
                                                                                                                                                                          N-linked
                                                                                                                                                                                       Potential
                                                                                                                                                                                                      Cleavage
                                                                                                                                                                                                                  Poly-Pro.
                                                                                                                                                                                                                              Pro-rich.
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                                                                                                                                                                                                                                                      Signal-anchor for type protein (Potential)
                                                                                                                                                                                                                                                                                                                        member
                                                                                                                                                                                                                                                                                                                                   Tumor necrosis factor ligand superfamily
                                                                                                         FTId=VSP 006443
                                                                                                                                                                                                                                                                                                                        6, membrane
                                                                                                                                             (GlcNAc...)
(GlcNAc...)
(GlcNAc...)
                                                                                                                                                                                                                                                                                                      cane form.
factor ligand superfamily
                                                                                                                                  ATPVHPLKKRS
           binding
                                                                                                                                                           (Potential).
                                                                                                                                                                                                                                                                                                                                                                 Glycoprotein;
                                                                                                                                              (Potential)
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           TNRFSF6
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| Query Match 12.6%; Score 186; DB 1; Length 281; Best Local Similarity 22.1%; Pred. No. 4.9e-07; |
|---|
| Matches 63; Conservative 54; Mismatches 82; Indels  |
| Qy 4 MEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE                                  |
| Db 71 LKKRGNHSTG-LCLLVMFFMVLVALVGLGLGMFQLFHLQKELAELRESTSQMHTASSIEK                              |
| Qy 61 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120                          |
| Db 130 QIGHPSPPPEKKELRKV  |
| Qy 121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG                             |
| Db 147AHLTGKSNSRSMPLEWEDT-YGIVILSGVKYKKGGLVINETG 187  |
| QY 181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIY-KYTSYPDPILLMKSARNSCWSK                                   |
| Db 188 LYFVYSKVYFRGQSCNNLPLSHKVYMRNSKYPQDLVMMEGKMMSYCTTGQMWAR                                   |
| Qy 234 DAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGI   |
| Db 242SYLGAVFNLTSADHLYVNVSELSLVNFEESQTFFGLY 279   |

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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Title:
Perfect score:
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seq length: 2000000000
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1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep:*

2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*

3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*

4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*

5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*

6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*

7: /cgn2_6/ptodata/2/paa/US11_NEW_COMB.pep:*

8: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*
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Match
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    181127 seqs, 44957854 residues
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Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-077-435-1
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US-11-028-780-22
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US-97-91-1538-157
US-97-91-1538-157
US-97-91-1538-157
US-11-028-780-38
US-11-028-780-38
US-11-028-780-34
US-10-916-286A-73
US-10-916-286A-73
US-10-916-286A-73
US-11-028-780-10
US-11-028-780-11
US-11-028-780-11
US-11-043-770-1155
US-11-043-770-1155
US-11-043-770-1155
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Sequence 1, Appli
Sequence 20, Appli
Sequence 4, Appli
Sequence 52, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 38, Appli
Sequence 38, Appli
Sequence 36, Appli
Sequence 37, Appli
Sequence 73, Appli
Sequence 136, Appli
Sequence 136, Appli
Sequence 136, Appli
Sequence 137, Appli
                                                                                                                                                                                                                                                                                                                                                                                                     Description
   US-11-028-780-20

US-11-028-780-20

; Sequence 20, Application US/11028780

; GENERAL INFORMATION:
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| B   | Q Q Q  | US CS  |  |
|---|--|--|--|
|   | Query<br>Best<br>Match   | 26 27 28 29 29 29 30 30 30 31 31 31 31 31 31 31 31 31 31 31 31 31  |  |
| 121  <br>121  <br>181  <br>181  <br>241 :                                     | 1 1 1 61 61  | 26 125.5<br>27 125.5<br>28 122<br>29 122<br>30 122<br>31 122<br>31 122<br>32 122<br>33 122<br>34 123<br>36 119.5<br>37 119.5<br>38 119.5<br>39 116.5<br>40 117.1<br>41 116.5<br>42 116.5<br>43 116.5<br>44 116.5<br>45 116.5<br>47 116.5<br>48 116.5<br>49 116.5<br>40 117.1<br>10 077-435-1<br>PRIOR APPLICURENT PILLING ENERGY PILLING PERFORMANT PILLING PERFORMANT |  |
| RVAAHITG  | Similarity 1; Conserving MAMMEVQGGI MAMMEVQGGI MAMMEVQGGI DDSYMDPNDE   | 26 125.5 8.5 27 125.5 8.5 28 122 8.3 28 122 8.3 30 122 8.3 31 122 8.3 31 122 8.3 33 122 8.3 34 122 8.3 35 119.5 8.1 36 119.5 8.1 37 118 8.0 38 118 8.0 39 117 7.9 40 117 7.9 41 116.5 7.9 42 116.5 7.9 43 116.5 7.9 44 116.5 7.9 45 116.5 7.9 47 116.5 7.9 48 116.5 7.9 49 116.5 7.9 49 116.5 7.9 40 117 7.9 41 116.5 7.9 42 116.5 7.9 43 116.5 7.9 44 116.5 7.9 45 116.5 7.9 46 116.5 7.9 47 116.5 7.9 48 116.5 7.9 49 116.5 7.9 49 116.5 7.9 49 116.5 7.9 49 116.5 7.9 49 116.5 7.9 49 116.5 7.9 49 116.5 7.9 49 116.5 7.9 49 116.5 7.9 49 116.5 7.9 49 116.5 7.9 49 116.5 7.9 49 116.5 7.9 49 116.5 7.9 49 116.5 7.9 49 116.5 7.9 49 116.5 7.9 49 116.5 7.9 40 116.5 7.9 41 116.5 7.9 41 116.5 7.9 42 116.5 7.9 43 116.5 7.9 44 116.5 7.9 45 116.5 7.9 46 116.5 7.9 47 116.5 7.9 48 116.5 7.9 49 116.5 7.9 49 116.5 7.9 49 116.5 7.9 40 116.5 7.9 41  |  |
| GTRGRSNTLS GTRGRSNTLS GTRFGRSNTLS TYFRFOESIK FILLENDRIF FELKENDRIF FELKENDRIF | 100 larity 100 Conservative MEVGGPSLGQTV MEVGGPSLGQTV MEVDGGPSLGQTV MEVDFUDEESMNSI   |  |  |
| TLSS  | SPCW   | 3 P802 BH 0 76655667171777776887   |  |
| .VAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHS<br>                                | Score 1478; DB ; Pred. No. 4.1e- o; Mismatches IVIFTVLLQSLCVAVTYV              IVIFTVLLQSLCVAVTYV VIVIFTVLLQSLCVAVTYV                IVIFTVLLQSLCVAVTYV QVKWQLRQLVRKMILRTS | 33 7 US-11-054-539-3 33 8 US-60-643-337-4 44 6 US-10-839-694A-3 105 7 US-11-028-780-2 105 7 US-11-033-545-304 105 7 US-11-054-539-4 117 1 PCT-US05-02350-1146 117 7 US-11-043-770-1146 117 1 US-11-043-770-137 140 1 PCT-US05-02350-137 140 7 US-11-043-770-137 140 7 US-11-043-770-137 150 1 PCT-US05-02350-326 157 6 US-10-839-694A-5 157 6 US-10-839-694A-2 157 6 US-10-697-628B-9 157 6 US-10-954-900A-9 157 6 US-10-954-900A-9 157 7 US-11-053-750-1  ALIGNMENTS  US/10077435  US/10077435  US/10077435  US/10077435  US-10-696-628B-9 158: US-60/269,698   |  |
| SSRSGHSFLSNLHLRNGELVIHEKG 180   | 16; Length 281; 129; Indels 0; Gaps 0; 0; Indels 0; Gaps 0;  | Sequence 3, Appli<br>Sequence 4, Appli<br>Sequence 204, Appli<br>Sequence 2, Appli<br>Sequence 4, Appli<br>Sequence 1146, Ap<br>Sequence 1146, Ap<br>Sequence 137, App<br>Sequence 137, App<br>Sequence 326, App<br>Sequence 5, Appli<br>Sequence 5, Appli<br>Sequence 9, Appli<br>Sequence 9, Appli<br>Sequence 9, Appli<br>Sequence 1, Appli<br>Sequence 9, Appli<br>Sequence 9, Appli<br>Sequence 1, Appli<br>Sequence 1, Appli<br>Sequence 1, Appli<br>Sequence 1, Appli<br>Sequence 1, Appli  |  |

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APPLICANT: Li, Yuling
APPLICANT: Oren, Deena
APPLICANT: Arnold, Edward
APPLICANT: Arnold, Edward
APPLICANT: Volovik, Yulia
TITLE OF INVENTION: Crystalline Neutrokine-alpha Pro
TITLE OF INVENTION: Thereof, and Method of Use Ther
FILE REFERENCE: PF567
CURRENT APPLICATION NUMBER: US/10/839,694A
CURRENT APPLICATION NUMBER: PCT/US02/35661
PRIOR APPLICATION NUMBER: 60/331,049
PRIOR FILING DATE: 2001-11-07
PRIOR APPLICATION NUMBER: 60/331,049
PRIOR FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 18
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SEQ ID NO 20
LENGTH: 281
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Best Local Similarity
                                                                                                                                                                                                                 SEQ ID NO 4
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TITLE OF INVENTION: Heteromultimeric TNF Ligand Family members
FILE REFERENCE: PF559C1
CURRENT APPLICATION NUMBER: US/11/028,780
CURRENT FILING DATE: 2005-01-05
PRIOR APPLICATION NUMBER: 10/202,062
PRIOR FILING DATE: 2002-07-25
PRIOR FILING DATE: 2002-07-25
PRIOR FILING DATE: 2002-07-25
PRIOR FILING DATE: 2002-07-25
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PRIOR FILING DATE: 2001-07-27
NUMBER OF SEQ ID NOS: 42
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                                                          NAME/KEY: MISC_FEATURE
LOCATION: (15)...(15)
OTHER INFORMATION: Xaa equals
OTHER INFORMATION: Figure 1
                                                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                                                                              LENGTH: 163
TYPE: PRT
NAME/KEY: MISC_FEATURE LOCATION: (16)..(16)
                                                                                                                                        FEATURE:
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Pred. No. 4.
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RESULT 4
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SOPTWARE: PatentIn version 3.2
SEQ ID NO 22
LENGTH: 317
                                                                                                                                                                                                                   Sequence 22, Application US/11028780 GENERAL INFORMATION:
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Best Local (
                                             APPLICANT: Human Genome Sciences, Inc.,
TITLE OF INVENTION: Heteromultimeric TNF Ligand Family members
FILE OF INVENTION UNDER: US/11/028,780
CURRENT APPLICATION NUMBER: US/11/028,780
CURRENT FILING DATE: 2005-01-05
PRIOR APPLICATION NUMBER: 10/202,062
PRIOR APPLICATION NUMBER: 10/202,062
PRIOR PILING DATE: 2002-07-25
PRIOR PILING DATE: 2002-07-25
PRIOR APPLICATION NUMBER: 60/307,838
PRIOR APPLICATION NUMBER: 60/307,838
PRIOR FILING DATE: 2001-07-27
NUMBER OF SEQ ID NOS: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: MISC_FEATURE IOCATION: (23)...(23)
OTHER INFORMATION: Xaa equals Ser omitted at asterisk in TRAIL sequence OTHER INFORMATION: Figure 1
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LOCATION: (22)...(22)
OTHER INFORMATION: Xaa equals
OTHER INFORMATION: Figure 1
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LOCATION: (19) ...(19)
OTHER INFORMATION: Xaa equals
OTHER INFORMATION: Figure 1
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LOCATION: (18)..(18)
OTHER INFORMATION: Xaa equ
OTHER INFORMATION: Figure
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OTHER INFORMATION: Figure 1
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Local Similarity 94.5%;
nes 154; Conservative
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Pred. No. 6.2e-68;
0; Mismatches 9
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RESULT 6
US-10-839-694A-6
; Sequence 6, Application US/10839694A
; GENERAL INFORMATION:
; APPLICANT: Li, Yuling
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PRIOR FILING DATE: 2000-02-23
NUMBER OF SEQ ID NOS: 166
SOFTWARE: Patentin version 3.2
SEQ ID NO 157
LENGTH: 170
TYPE: PRT
ORGANISM: Homo sapiens
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US-11-028-780-22
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APPLICANT: Hitz, Anna
APPLICANT: Boyle, William J.
APPLICANT: Sullivan, John K.
TITLE OF INVENTION: SELECTIVE BINDING AGENTS OF OSTEOPROTEGERIN BINDING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: A-633A
CURRENT APPLICATION NUMBER: US/09/791,153E
CURRENT FILING DATE: 2001-02-22
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Local Similarity 24.1%; Pred. No. 1.2e-15;
nes 71; Conservative 61; Mismatches 117;
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                                                                                                                                                                                                                                   LYANICFRHHETSGDLATEYLOLMVYVVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSI
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                                                                                                                                                                                                                                                                                                                                                                                                                 15.6%; Score 230.5; DB 5; 34.2%; Pred. No. 4.6e-14;
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APPLICANT: Human Genome Sciences, Inc.,
ITILE OF INVENTION: Heteromultimeric TNF Ligand Family members
FILE REFERENCE: PF559C1
CURRENT APPLICATION NUMBER: US/11/028,780
CURRENT FILING DATE: 2005-01-05
PRIOR APPLICATION NUMBER: 10/202,062
PRIOR FILING DATE: 2002-07-25
PRIOR FILING DATE: 2002-07-25
PRIOR APPLICATION NUMBER: 60/307,838
PRIOR APPLICATION NUMBER: 60/307,838
PRIOR FILING DATE: 2001-07-27
NUMBER OF SEG ID NOS: 42
SOFTWARE: Patentin version 3.2
SEGUID NO 12
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SEQ ID NO 6
LENGTH: 155
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 15.5%; Score 228.5; DB 6; Length 155; Best Local Similarity 34.2%; Pred. No. 6.3e-14; Matches 54; Conservative 31; Mismatches 62; Indels 11
                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                            Query Match
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CURRENT FILING DATE: 2004-05-06
PRIOR APPLICATION NUMBER: PCT/US02/35661
PRIOR APPLICATION NUMBER: PCT/US02/35661
PRIOR PILING DATE: 2002-11-07
PRIOR APPLICATION NUMBER: 60/331,049
PRIOR FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 18
NUMBER OF SEQ ID NOS: 18
                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 281
TYPE: PRT
ORGANISM: human
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                     121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   114 NVGGFFKLRAGEEÍSIQVSNPSLLDPDQDATYFGAFKV 151
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                                                                                              130 QIGHPSPPPE-----KKELRKV-----
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                                                                                                                                                                                                                                                                                               63;
                                                                                                                                           61 DDSYMDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
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                                                                                                                                                                                                                                             4 MEVQGGPSLGQTCVLIVIFTVLLQSLCVAV---TYVYFTNELKQMQDKYSKSGIACFLKE
                                                                                                                                                                                                LKKRGNHSTG-LCLLVMFFMVLVALVGLGLGMFQLFHLQKELAELRESTSQMHTASSLEK 129
---AHLT---GKŚNSRŚMP------LEWEDT-YGIVLLSGVKYKKGGLVINETG 187
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Volovik, Yulia
                                                                                                                                                                                                                                                                                            12.6%; Score 186; DB 7; Length 281; ilarity 22.1%; Pred. No. 1.1e-09; Conservative 54; Mismatches 82; Indels
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US-11-054-539-6
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PRIOR APPLICATION NU
PRIOR FILING DATE: 2
PRIOR APPLICATION NU
PRIOR FILING DATE: 2
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LENGTH: 281
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Best Local Similarity
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PRIOR FILING DATE: 2004-02-11
PRIOR APPLICATION NUMBER: 60/580,387
PRIOR FILING DATE: 2004-06-18
PRIOR APPLICATION NUMBER: 60/617,191
PRIOR FILING DATE: 2004-06-18
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PRIOR APPLICATION NUMBER: 60/330,835
PRIOR FILING DATE: 2001-10-31
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CURRENT FILING DATE: 2005-02-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Remaining Prior Application data removed - See File Wrapper or PALM NUMBER OF SEQ ID NOS: 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/336,726 FILING DATE: 2001-12-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/368,548 FILING DATE: 2002-04-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 10/270,487 FILING DATE: 2002-10-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 2003-12-19
APPLICATION NUMBER: 10/735,865
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                                                                                                                                                                           147
    242
                                      234 DAEYGLYSIYQGGIFELKENDRIFYSYTNEHLIDMDHEASFFGAF 278
                                                                                     188
                                                                                                                         181 FYYIYSQTYFRFQEEIKENTKNDKQMVQYIY-KYTSYPDPILLMKSARNS-----CWSK 233
                                                                                                                                                                                                                    121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
                                                                                                                                                                                                                                                              130 QIGHPSPPPE-----KKELRKV-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181
                                                                                                                                                                                                                                                                                                       61 DDSYMDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                     63;
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                                                                                                                                                                                                                                                                                                                                             LKKRGNHSTG-LCLLVMFFMVLVALVGLGLGMFQLFHLQKELAELRESTSQMHTASSLEK 129
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                                                                                     LYFVYSKVYFRGQ-----SCNNLPLSHKVYMRNSKYPQDLVMMEGKMMSYCTTGQMWAR
                                                                                                                                                                         ---AHLT---GKSNSRSMP------LEWEDT-YGIVLLSGVKYKKGGLVINETG 187
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SSYLGAVENLISADHLYVNVSELSLVNFEESQTFFGLY 279
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                                                                                                                                                                                                                                                                                                                                                                                                                                   12.6%; Score 186; DB 7; Length 281; 22.1%; Pred. No. 1.1e-09; tive 54; Mismatches 82; Indels
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                                                                                     241
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RESULT

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NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
; LENGTH: 251
; TYPE: PRT
; ORGANISM: human
US-11-028-780-38
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                                                                                                                                                                                                                                                             ; TYPE: PRT; ORGANISM: human US-11-028-780-36
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                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn version 3.2
SEQ ID NO 36
LENGTH: 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 36, Application US/11028780
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.,
TITLE OF INVENTION: Heteromultimeric TNF Ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 38, Application US/11028780 GENERAL INFORMATION:
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                                                                                                                                                                               Matches
                                                                                                                                                                                              Query Match 10.8%; Score 160; DB 7; Best Local Similarity 35.3%; Pred. No. 1.6e-07;
                                                                                                                                                                                                                                                                                                                                                                                                      PILE REFERENCE: PF559C1
CURRENT APPLICATION NUMBER: US/11/028,780
CURRENT FILING DATE: 2005-01-05
PRIOR APPLICATION NUMBER: 10/202,062
PRIOR FILING DATE: 2002-07-25
PRIOR APPLICATION NUMBER: 60/307,838
PRIOR APPLICATION NUMBER: 60/307,838
PRIOR FILING DATE: 2001-07-27
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CURRENT APPLICATION NUMBER: US/11/028,780
CURRENT FILING DATE: 2005-01-05
PRIOR APPLICATION NUMBER: 10/202,062
PRIOR FILING DATE: 2002-07-25
PRIOR FILING DATE: 2002-07-25
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          101
                                                                                                                                  154 WESSRSGHSFLSN-LHLRNGELVIHEKGFYYIYSQTYFRFQ----EEIKENTKNDK--QM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    107 QQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNE-KALGRKINSWESSRSGHSFLS 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82
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TVVİTKVTDSYPBPTQLLMGTKSVC-----EVGSNWFQPIYLGAMPSLQBGDKLMVNVSD
                                                 VQYIYKYT-SYPDPILLMKSARNSCWSKDAEYG---LYSIYQGGIFELKENDRIFVSVTN 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DPILLMKSARNSCWSKDAEYG---LYSIYQGGIFELKENDRIFVSVTNEHLIDMDHE-AS
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                                                                                                                                                                             Conservative 24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -EVGSNWFQPIYLGAMPSLQEGDKLMVNVSDISLVDYTKEDKT 244
                                                                                                                                                                                                                      DB 7; Length 174;
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US-11-028-780-34
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                                                                                        ; ORGANISM: Felia catus US-10-916-286A-73
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SEQ ID NO 34
LENGTH: 240
TYPE: PRT
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GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.,
TITLE OF INVENTION: Heteromultimeric TNF Ligand Family members
                                                                                                                                                       SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 73
LENGTH: 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 73, Application US/10916286A GENERAL INFORMATION:
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Best Local Similarity 23.8%; Pred. No. 2.6e-07;
Matches 53; Conservative 41; Mismatches 66
Query Match 10.1%; Score 149.5; DB 6; Best Local Similarity 24.4%; Pred. No. 2.4e-06; Matches 69; Conservative 57; Mismatches 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: human
-11-028-780-34
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                                                                                                                                                                                                                                                                                     APPLICANT: Dreitz, Matthew J.

TITLE OF INVENTION: CANINE IL-4 IMMUNOREGULATORY PROTEINS AND USES THEREOF
FILE REFERENCE: IM-2-C1-R
CURRENT APPLICATION NUMBER: US/10/916,286A
CURRENT FILING DATE: 2004-08-11
PRIOR APPLICATION NUMBER: 09/322,409
PRIOR FILING DATE: 1999-05-28
PRIOR FILING DATE: 1999-05-28
                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/087,306
PRIOR FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 154
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                                                                                                                                       TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VQLGGVGCPLGLASTITHGLYKRTPRYPEELELLVSQQSPCGRATSSSRVW 197
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    Indels
                                              260;
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    43;
  Gaps
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US-10-916-286A-65
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APPLICANT: Dreitz, Matthew J.
APPLICANT: Dreitz, Matthew J.
TITLE OF INVENTION: CANINE IL-4 IMMUNOREGULATORY PROTEINS AND USES THEREOF
FILE REFERENCE: IM-2-C1-R
CURRENT FILING DATE: 1204-08-11
PRIOR APPLICATION NUMBER: 09/322,409
PRIOR APPLICATION NUMBER: 09/322,409
PRIOR APPLICATION NUMBER: 309-05-28
PRIOR FILING DATE: 1999-05-28
PRIOR FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 154
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 65
LENGTH: 260
TYPE: DET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               115
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                        234 DAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFG 276
                                                                                            160 LAVKRQGLYYVYAQVTFCSNRA----ASSQAPFVASLCLHSPSGTERVLLRAASSRGSSK
                                                                                                                                           174 LVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSK 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       216 PC--GQQSIHLGGVFELHPGASVFVNVTDPSQVSHGTGFTSFG 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                160 LAVKROGLYYIYAQVTFCSNRE----ASSQAPFIASLCLHSPSGSERVLLRAANARSSSK 215
                                                                                                                                                                                                                                                                                    68 ---TLOKCNKGEGSLSLLNCEEIKSOFEAFLKEIMLNNE-----MKKBENIA---MQK 114
                                                                                                                                                                                                                                                                                                                              60 EDDSYWDPNDEESMNS--PCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRER 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68 ---TLOKCNKGEGALSLINCEEIKSRFEAFLKEIML--NKET-----KKEKNVA---MOK 114
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                                                                                                                                                                                                                                                                                                                                                                                                                             2 AMMEYQGGPSLGQTCVLIVIFTVLL--QSLCVAVTYVYFTNELKQMQDKYSKSGIACFLK 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                  APRSVATGPPVSMK-IFMYLLTVFLITQMIGSALFAVYLHRRLDKIEDERNLYEDFVFMK 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DAEYGLYSIYQGGIFELXENDRIFVSVTNEHLIDMDHEASFFG 276
                                                                                                                                                                                          GDQDPRIAAHVI----SEASSNPAS-----VLRW-APKGYYTISSNLVSLENGKQ
                                                                                                                                                                                                                                  GPQ--RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNL-HLRNG-E 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GDQDPRVAAHV-----ISEASSSTASVL----QW-APKGYYTISSNLVTLENGKQ 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AMMEVQGGPSLGQTCVLIVIFTVLL--QSLCVAVTYVYFTNELKQMQDKYSKSGIACFLK
PC--GQQSIHLGGVFELHPGASVFVNVTDPSQVSHGTGFTSFG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10.0%; Score 147.5; DB 6; 24.0%; Pred. No. 3.7e-06; ative 55; Mismatches 117;
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RESULT 14
PCT-US05-02350-136
; Sequence 136, Application PC/TUS0502350
; GENERAL INFORMATION:

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; Sequence 143, Application US/11021951
; GENERAL INFORMATION:
   APPLICANT: HAUFTS, ULTICH
; APPLICANT: KOLTERMANN, Andre
; APPLICANT: KOLTERMANN, Andre
; APPLICANT: COTSMEIER, Christian
; APPLICANT: Kettling, Ulrich
; APPLICANT: Kettling, Ulrich
; APPLICANT: COCO, Wayne Michael
; TITLE OF INVENTION: New Biological Entities And Th
; TITLE OF INVENTION: And Diagnostic Use Thereof
; FILE REFERENCE: 04156,0002U5
                                                                                                                                                                                                                                                                                                                                               US-11-021-951-143
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Best Local S
Matches 66
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SEQ ID NO 136
LENGTH: 261
TYPE: PRT
ORGANISM: Homo sapiens
CURRENT APPLICATION NUMBER: US/11/021,951
CURRENT FILING DATE: 2004-12-22
PRIOR APPLICATION NUMBER: 10/872,198
PRIOR FILING DATE: 2004-06-18
PRIOR APPLICATION NUMBER: 60/543,518
PRIOR FILING DATE: 2004-02-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Pollock, Sarah
APPLICANT: Savitsky, Kinneret
APPLICANT: Bernstein, Jeanne
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES ENCODING POLYPEPTIDES AND METHODS USING
TITLE OF INVENTION: SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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CURRENT FILING DATE: 2005-02-10
NUMBER OF SEQ ID NOS: 1155
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56; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ERSLSLLNCEEIKSOFEGFVKDIML-NKEET----KKENSFEMQKGDQNPQ-IAAHV-- 126
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Rosenberg, Avi
Dahary, Dvir
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Toporik, /
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Cojocaru, Gad S.
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Diber, Alex
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Galit
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SEQ ID NO 143
LENGTH: 261
TYPE: PRT
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PRIOR FILLING DATE: 2003-11-25
PRIOR APPLICATION NUMBER: EP 04003058
PRIOR FILLING DATE: 2004-02-11
PRIOR APPLICATION NUMBER: EP 03025871
PRIOR FILLING DATE: 2003-11-11
PRIOR APPLICATION NUMBER: EP 03025851
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PRIOR FILING DATE: 2003-06-18
NUMBER OF SEQ ID NOS: 191
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GQQSIHLGGVFELQPGASVFVNVTDPSQVSHGTGFTSFG
                          GLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFG
                                                                                           AQVTFCSNREASSQAPFIASLCLKSPGRFER-------ILLRAANTHSSAKPC--
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                                                                                                                                       SQTYFRFQEEIKENT-----KNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEY
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| ADK72296           | ADK72304           | ADK72303           | ADK72311           | ADE76953           | ABW02276           | ADD19010           | ADD14080 | ADC35202 | ADB61471           | ABO25125 | AA031151           | AAE36258 | ABP60546 | ABG71905           | ABR42313           | ABU08558           | AA029543 | ABG72738           | ABU71443           |
| Adk72296 Human wil | Adk72304 Human Apo | Adk72303 Human Apo | Adk72311 Human Apo | Ade76953 Human pro | Abw02276 Human TRA | Add19010 Human dis | Human    | . Human  | Adb61471 Native hu | Human    | Aao31151 Human TNF | Human    | Human    | Abg71905 Human TRA | Abr42313 Human TRA | Abu08558 Human TNF | Human    | Abg72738 Human TNF | Abu71443 Human neo |

ALIGNMENTS

## RESULT 1 AAW1977 ID AAW1977 ID AAW17 ID AAW17 XX AC AAW1 XX DT 22-S XX DT 22-S XX DT Wove XX DT Wov WPI; 1997-372867/34. N-PSDB; AAT72796. Region Region AAW19777; AAW19777 standard; protein; 281 AA Ashkenazi AJ, Chuntharapai A, 09-JAN-1996; 08-JAN-1997; 17-JUL-1997. WO9725428-A1. Protein Modified-site Region Protein Protein Homo sapiens. Apo-2 ligand; cytokine; apoptosis; breast cancer; colon cancer; therapy. Novel cytokine Apo-2 ligand. 22-SEP-1997 Peptide (GETH ) GENENTECH INC (first entry) 96US-00584031 /note= "Claim 2" 41. .281 97WO-US000272. /label= Glycosylation /note= "putative N-linked glycosylation site" 114. 281 /note= "Claim 1" Location/Qualifiers 'label = Cytoplasmic\_region 'note= "Claim 4" label= Extracellular\_region label = Transmembrane\_region note= . 281 ote= "Claim 3" .40 Kin ፭

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Best Local S
Matches 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A novel cytokine (AAW19777), designated Apo-2 ligand, induces mammalian cell apoptosis. It is belived to be a member of the tumour necrosis factor cytokine family. Its amino acid sequence was deduced from a CDNA clone (AAT72796) isolated from a human placental CDNA library. Apo-2 ligand polypeptides, esp. those corresponding to amino acids 114-281, 41-281, 15-281 or 1-281 of Apo-2 ligand, can be produced by culturing cells transformed or transfected with a vector contg. Apo-2 ligand nucleic acid. They can be used to induce apoptosis in mammals and to treat pathological conditions such as cancer (esp. breast or colon cancer) or to raise antibodies useful in diagnostic assays
                                                                                                                                                                                                                             Apoptosis inducing molecule-I; AIM-I; autoimmune disorder; tumour necrosis factor ligand superfamily; AIM-I altered e neoplasia inhibition; anti-inflammatory agent.
                                                                                                                                                                                                                                                                                                                                                                      AAW27134 standard;
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 N-PSDB; AAT85210
              WPI; 1997-470807/43.
                                                                                                                                                                                                                                                                                     Human Apoptosis
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                                                                                                                                                                                                                                                                                                                                           AAW27134;
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                                       Ruben SM;
                                                                                                                       14-MAR-1996;
                                                                                                                                                  18-SEP-1997.
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                                                                                              14-MAR-1996;
                                                                   (HUMA-) HUMAN
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                                                                   GENOME SCI INC
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Pred. No. 3.8e-137;
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Best Local Similarity
Matches 281; Conserv
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  Domain
                                                       Domain
                                                                                                                                                                                                                                                 Tumour necrosis factor related apoptosis inducing ligand; TRAIL; cytokine; cancer; leukaemia; lyphoma; melanoma; viral infection; thrombotic microangioplasty; therapy.
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nilarity 100.0%;
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/label= Cytoplasmic_domain
19. .38
/label= Transmembrane_domain
39. .281
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Pred. No. 3.8e-137;
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Matches 281;
                                                                                                                                                                                                                                                                                                                                          Human tumour necrosis factor related apoptosis inducing ligand (TRAIL) (AAW19787) is a novel cytokine that induces apoptosis of certain target cells, including cancer cells and virally infected cells. Its amino acid sequence was deduced from cDNA clone HuAIC (AAT72848), deposited in vector pDC409 as ATCC 69849. Recombinant TRAIL polypeptides (esp. soluble polypeptides) can be expressed in host cells and used in the treatment of cancer (e.g. leukaemia, lymphoma and melanoma) and viral infections, or
                                                                                                                                                                                                                                                                                                     Sequence 281 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 10; Page 43-44; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                TRAIL, a novel cytokine, induces apoptosis in cancer and virus-infected cells - useful for treating thrombotic microangiopathy, cancer and viral
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01-NOV-1995;
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                   AAW76829 standard; protein; 281
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                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                 raise antibodies that may be useful for treating thrombotic
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                                                                                                       FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCMSKDABYGLY
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95US-00548368.
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89. .90
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109. .1
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Pred. No. 3.8e-137;
); Mismatches 0;
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Query Match
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09-MAY-1997;
22-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence represents the human tumour necrosis factor (TNF)-related receptor, TL2 (also known as tumour necrosis factor-related apoptosis-inducing ligand, TRAIL). This protein is used in a method resulting in the isolation of the novel human TNF related receptor, TR6. TR6 polypeptides and polynucleotides can be used in the treatment of chronic and acute inflammation, arthritis, septicaemia, autoimmune diseases (e.g. inflammatory bowel disease, psoriasis), transplant rejection, graft vs. host disease, infection, stroke, ischaemia, acute respiratory disease syndrome, restenosis, brain injury, (acquired autoimmune disease syndrome) AIDS, bone diseases, cancer (e.g. lympho-proliferative disease), atherosclerosis and Alzheimers disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 32-33; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA encoding tumour necrosis factor receptor TR6 polypeptide, antibody, agonist, antagonist, etc.
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                                     SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG
                                                                                                          FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY
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SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG
                                                                                                                                          FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY
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97US-00853684.
97US-00916625.
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                                                                                                                                                                                                                                  This represents a human tumour necrosis factor related apoptosis ligand (TRAIL) polypeptide. The human and murine TRAIL polypeptides can induce apoptosis of Jurkat cells. The encoding nucleic acid sequences are useful for producing the recombinant TRAIL polypeptides, which may be useful in studies of apoptosis, to purify leukaemia, lymphoma or melanoma cells (e.g. to isolate antigens for vaccine development). The polypeptides can be used to treat leukaemia, lymphoma or melanoma (e.g. by extracorporeal treatment of blood or bone-marrow), or to treat viral infections
                                                                                                                                                                                                             Sequence 281 AA;
                                                                                                                                                                                                                                                                                                                                                          Claim 1; Col 33-36; 28pp; English.
                                                                                                                                                                                                                                                                                                                                                                                  DNA encoding cytokine TNF-related apoptosis ligand polypeptides for producing recombinant polypeptides for research and therapy leukaemia, lymphoma, melanoma and viral infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1998-347322/30.
N-PSDB; AAV29518.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Goodwin RG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-JUN-1995;
01-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-JUN-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tumour necrosis factor related apoptosis ligand; TRAIL; research; human; cytokine; therapy; leukaemia; lymphoma; melanoma; viral infection.
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             RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
                                                                                                                  MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
                                                               DDSYMDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ
                                                                                                      MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
                                                   DDSYMDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ
                                                                                                                                                         100.0%; ilarity 100.0%; Conservative 0
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95US-00548368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note= "transmembrane region"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "extracellular domain"
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                                                                                                                                                         Score 1478; DB 2;
Pred. No. 3.8e-137;
; Mismatches 0;
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                                                           Query Match
Best Local S
Matches 281
                                                                                                                                                               The present sequence represents human AGP-1 is a tumour-necrosis cactor (TNR)-related protein, involved in inflammation, myelopolesis and bone resorption. It has the same nucleic acid and amino acid (aa) sequences as the TNF-related apoptosis-induced ligand (TRAII) described In Immunity, 3 (1995) 673. Antibodies (Ab) are used as immunoassay reagents for detecting AGP-1 expression. Nucleic acid complementary to CRAP-1 is used to regulate AGP-1 expression and antagonistic compounds are used to treat inflammation (e.g. rheumatoid arthritis, systemic lupus crythematosus, psoriasis, scleroderma, infection-related inflammation) or complementary to compression of diseases (e.g. osteopycosis, osteomyelltis, hypercalcaemia, Paget's disease). AGP-1 can be used to treat haematopoletic diseases associated with reduction in the number of bone marrow cells, particularly neutrophils and lymphocytes, e.g. where caused by disease, injury or exposure to myelosuppressive agents. Host cells, transformed with expression vectors containing AGP-1 DNA, are used to
                                                                                                                        Sequence 281 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acid encoding AGP-1, a tumour necrosis factor-related protein useful for treating inflammation, bone resorption and haematopoietic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Johnson MJ, Simonet
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                                                                                                                                                     produce recombinant
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                                                                           Local Similarity
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                MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
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Pred. No. 3.8e-137;
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                                                                                        Length 281;
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Best Local Similarity
Matches 281; Conserv
                                                                                             The specification describes the use a polypeptide corresponding to at least the primary sequence of part of the present sequence to produce a diagnostic, prophylactic or therapeutic composition useful in cases of degenerative, autoimmune and inflammatory diseases. The polypeptides can be used in treatment of neurodegenerative disease, lupus erythematosus, rhuematoid arthritis, and SEP, The polypeptides are apoptotic in central nervous system cells, antigenic and specifically recognise the surface receptor of the TRAIL protein. The polypeptide is a marker of disease and a therapeutic target, e.g. its apoptotic activity can be blocked with an anti-TRAIL antibody or a TRAIL equivalent that binds to specific receptors, inhibiting formation of natural complex
                                                                                                                                                                                                                                                                                                                                                   Use of polypeptide derived from TRAIL protein for diagnosis of degenerative disease - autoimmunity and inflammation, also useful in prevention or treatment, and similar use of corresponding ligand and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-AUG-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neurodegenerative disease; autoimmune disease; inflammatory disease; lupus erythematosus; rhuematoid arthritis; SEP; apoptotic; surface receptor; TRAIL protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein associated with neurodegenerative and autoimmune diseases.
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                                                                   Sequence 281 AA;
                                                                                                                                                                                                                                                                                                     Claim 2; Page 13; 21pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-156177/14.
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                                                                                                                                                                                                                                                                                                                                      acid.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Belliveau JF,
 100.0%; Score 1478; DB 2; ilarity 100.0%; Pred. No. 3.8e-137; Conservative 0; Mismatches 0;
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MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE

60

Query Match Best Local S Matches 281

Local Similarity

100.0%; Score 1478; DB 2; ilarity 100.0%; Pred. No. 3.8e-137; Conservative 0; Mismatches 0;

Length Indels

281;

0

Gaps

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RESULT 8
AAX27012
ID AAX27
XX AAX2
XX Huma
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                                                       This sequence represents a novel human cytokine, designated Apo-21 ligand (Apo-21). The Apo-21 polypeptide can be produced by standard recombinant methodology. Apo-21 is useful for inducing apoptosis in mammalian cancer cells. This is useful for the treatment of cancer. Apo-21 can be used to induce apoptosis for pathological conditions characterized by decreased levels of apoptosis, e.g. autolmmune disorders like lupus and immune-mediated glomerular nephritis and cancer. Apo-21 and its nucleic acid coding sequence can also be used in quantitative and screening diagnostic techniques. Anti-Apo-21 antibodies can be used for treating diseases associated with increased apoptosis
   Sequence
                                                                                                                                                                                                                                                                                                                                                                                           Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAX86987.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     in mammalian cancer cells.
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15-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              novel cytokine, designated Apo-2 ligand, useful for inducing
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                                                                                                                                                                                                                                                                                                                                                                                           Fig 1A; 86pp; English.
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98US-00060533.
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                     This sequence is the human Apo-2 ligand protein, which is recognised by monoclonal antibodies produced by the hybridoma cell lines of the invention. The hybridoma cell lines are deposited under the American Type Culture Collection Accession Numbers: ATCC HB-12256, HB-12257, HB-12258 and HB-12259. The Apo-2 ligand antibodies may be used in diagnostic assays for Apo-2 ligand, e.g. detecting its expression in specific cells, tissues, or serum. The antibodies may also be employed as therapeutics. For instance, anti-Apo-2 ligand antibodies which block Apo-2 ligand activity, like Apo-2 ligand-induced apoptosis, may be employed to treat pathological conditions or diseases associated with increased apoptosis. They are also useful for the affinity purification of Apo-2 ligand from recombinant cell culture or natural sources. The Apo-2 ligand itself may be used to treat diseases e.g. cancer, by inducing apoptosis in cells
                                                                                                                                                                                                                        Claim 9; Fig la;
                                                                                                                                                                                                                                                               New isolated monoclonal antibodies having antigen specificity for Apoligand, e.g. 2G6, 2B11 or 5C2, useful for detecting the expression of -2 ligand serum, and for treating diseases associated with increased
                                                                                                                                                                                                                                                                                                                                                                                                                      09-JAN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           therapy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human Apo-2 ligand protein sequence
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                                                                                                                                                                                                                      46pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antibody; hybridoma cell line; diagnosis;
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RESULT 10
AAB24038
ID AAB24038
AC AAB24
XX AAB24
XX AAB24
XX AAB24
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XX Human
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Best Local Similarity
Matches 281; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-SEP-1999;
29-OCT-1999;
30-NOV-1999;
01-DEC-1999;
The present invention describes an antibody that binds to a human protein (I) selected from: PRO381; PRO1269; PRO1410; PRO1755; PRO1780; PRO3434; PRO340127; PRO3567; PRO1295; PRO1293; PRO1303; PRO4344; PRO4354; PRO4397; PRO40407; PRO1555; PRO1096; PRO2038; and PRO2262. (I) has anticancer activity and can be used to diagnose tumours in mammals, by detecting complex formation when the antibody is contacted with test cells. Increased expression of genes encoding (I) can also be detected to
                                                                                                                                                                                                                                                           Antibodies specific for
the growth of tumors in
polypeptide activity or
                                                                                                                                                                                                                Claim
                                                                                                                                                                                                                                                                                                                                                                      N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; TRAIL; tumour necrosis factor; TNF; diterpenoid triepoxide; TNF related apoptosis-inducing ligand; tumour cell; TRAIL receptor ligand; solid tumour; carcinoma; mammary carcinoma; non-small cell lung carcinoma.
                     Killing of tumor cells, e.g. solid tumors or carcinoma, comprises administration of synergistic combination of diterpenoid dispoxide tumor necrosis factor related apoptosis-inducing ligand.
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Matches 281;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; AGP-1; type II transmembrane protein; cytostatic; antiviral; antiinflammatory; hepatotropic; antiarteriosclerotic; anti-HIV; HIV; human immunodeficiency virus; apoptosis; proliferative disorder; can hepatitis; acquired immunodeficiency syndrome; AIDS; autoimmune disotransplant rejection; cardiovascular disease; arteriosclerosis.
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Best Local S
Matches 281
02-JUN-1999;
22-JUN-1999;
23-JUN-1999;
20-JUL-1999;
01-SEP-1999;
08-SEP-1999;
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                                                                                                                                                                                                        Human; PRO; cytostatic; nootropic; neuroprotective; respiratory general; antiinflammatory; antiangiogenic; immunosuppressive; immunostimulant; PRO agonist; cancer; inflammatory disorder; immunological disorder.
                                                                                                                           07-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pusion protein of AGP-1 protein and an Fc region, used to treat proliferative disorders, immune disorders, and virally-induced disorders.
                                                                                                 30-MAY-2000;
                                                                                                                                                      WO200073348-A2
                                                                                                                                                                                                                                                               Human PRO1096 protein.
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99WO-US012252.
99US-0140650P.
99US-0141037P.
99US-0144758P.
99WO-US020111.
99WO-US020594.
                                                                                                                                                                                                                                                                                                                                               protein; 281
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Pred. No. 3
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Matches 281;
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31-NOV-1999
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09-DEC-1999
16-DEC-1999
20-DEC-1999
20-DEC-1999
16-TEB-2000
11-FEB-2000
11-FEB-2000
02-MAR-2000
03-MAR-2000
03-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                     The present sequence is one of twenty eight novel PRO polypeptides. The PRO polypeptides and their agonists, including antibodies, peptides, and small molecule agonists, may be used to treat various tumours, e.g., cancers such as breast cancer, ovarian cancer, renal cancer, colorectal cancer, uterine cancer, prostate cancer, lung cancer, bladder cancer, central nervous system cancer, melanoma or leukaemia. They are also useful for treating other disorders such as neuronal, glial, astrocytal, hypothalamic and other glandular, macrophagal, epithelial, stromal and blastocoelic disorders, and inflammatory, angiogenic and immunological
                                                                                                                                                                                                                                                                                                                                 Sequence 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Twenty eight nucleic acids encoding PRO polypeptides which are useful treating various tumors, e.g. breast cancer, and other inflammatory, angiogenic and immunological disorders.
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17-MAY-2000;
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15-MAR-2000;
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               SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG
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                                                                                                           RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG
SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG
                                                     FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY
                                                                      FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY
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Smith
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99WO-US028313
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99WO-US0309551.
99WO-US03009576.
2000WO-US003565.
12000WO-US0034341.
2000WO-US005841.
2000WO-US005841.
2000WO-US006814.
2000WO-US00884.
2000WO-US008884.
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2000WO-US008884.
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Watanabe CK,
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O'connell
             18-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 281 AA;
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                                                           AAE11031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 6; Fig 1; 60pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Use of divalent metal ions for making Apo-2 ligand and in containing Apo-2 ligand for increasing yield and stability
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-JUN-2000; 2000WO-US017579
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                                                                                                                                                                                                                                                                                                                                                                                                                               present invention relates to a formulation comprising Apo-2 ligand idivalent metal ions. Apo-2 ligand and the formulation are useful for acting cancers and viral infections. Addition of divalent metal ions making Apo-2 ligand and formulations containing Apo-2 ligand results increased yield and stability of Apo-2 ligand trimers
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                                                                                                                    SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG
                                                                                                                                                                                FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY
                                                          standard;
                                                                                                                                                                  FYY I YSQTYFRFQEEIKENTKNOKQMVQY I YKYTSYPOPILLMKSARNSCWSKDAEYGLY
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                                                                                                                                                                                                                  TRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG
                                                          protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  divalent metal ions; viral infection; cancer
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Pred. No. 3.8e-137;
; Mismatches 0;
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Matches 281
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01-NOV-1995;
25-JUN-1996;
26-MAR-1998;
                                                                                                                                                                                                                                      The invention relates to a cytokine designated as tumour necrosis factor (TNF) related apoptosis inducing ligand (TRAIL), which induces apoptosis of certain target cells, including cancer cells and virally infected cells. The TRAIL polypeptides are useful in killing cancer cells, in treating viral infections (e.g. bovine viral diarrhoes or human immunodeficiency virus (HIV)) and cancers (e.g. leukaemia, lymphoma and melanoma), as a research reagent useful in studying apoptosis including the regulation of programmed cell death. TRAIL DNA sequences may be employed in developing a gene therapy approach to treating disorders mediated by defective or insufficient amounts of TRAIL, in the production of TRAIL polypeptides and as probes or primers in polymerase chain reactions (PCR). The present sequence is human TRAIL protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New tumor necrosis factor related apoptosis inducing ligand polypeptides for treating viral infections (e.g. bovine viral diarrhea or human immunodeficiency virus), or cancers (e.g. leukemia or lymphoma).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-595463/67.
N-PSDB; AAD18395.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; tumour necrosis factor; TNF; cytokine; cytostatic; virucide; TNF related apoptosis inducing ligand; TRAIL; cancer; viral infection human immunodeficiency virus; HIV; leukaemia; gene therapy; lymphoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 2; Col 45-48; 41pp; English.
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         RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG
                                                 DDSYMDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ
                                                                                             MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
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96US-00670354.
98US-00048641.
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Pred. No. 3.8e-137;
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RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG

| CY 181 FYELYSQIVERFQEELKENTKNDKQMVQXIYKTTSYPDFILLMKSA    | Search<br>Job tim                                  | рь  | Db Qy   |  |
|--|--|---|---|--|
| RNSCWSKDABYGLY 240<br>            <br>RNSCWSKDABYGLY 240 | completed: March 2, 2005, 14:47:40<br>e : 176 secs | 241 SIYQGGIFELKENDRIFYSYTNEHLIDMDHEASFFGAFLVG 281<br> | 181 FYYIYSOTYFRFQEEIKBNTKNDKOMVQYIYKYTSYDDIILMKSARNSCWSKDAEYGLY 240<br> |  |

OM protein - protein search, using sw model

Copyright

GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd

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; TYPE: amino a
; TOPOLOGY: lir
; MOLECULE TYPE:
US-08-670-354-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 1
US-08-670-354-2
                                                             TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/08670354
Patent No. 5763223
GENERAL INFORMATION:
                                                                                                         COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Macintosh

OPERATING SYSTEM: Apple 7.5.2

SOFTWARE: MICTOSOFT WORD:

APPLICATION NUMBER: US/08/670,354

FILING DATE: 25-UN-1996

CLASSIFICATION UMBER: US 08/496,632

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/496,632

FILING DATE: 29-UN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/548,368

FILING DATE: 01-NOV-1995

CLASSIFICATION: 435

APPLICATION NUMBER: US 08/548,368

FILING DATE: 01-NOV-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: ANGEREON, KAELYN A.

REFERENCE/DOCKET NUMBER: 2835-B

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 233-0644
                                                                                                                                                                                                                                                                                                                                                                                   STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Steven R. Wiley and APPLICANT: Raymond G. Goodwin. TITLE OF INVENTION: Cytokine That
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
                                                               281 amino acids
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US-09-569-611C-32
US-08-670-354-4
US-09-320-424-4
US-09-825-563-4
PCT-US96-10895-4
US-09-569-611C-31
US-09-569-6139-11
US-09-577-780-11
US-09-877-680-11
US-09-877-650-11
US-09-877-650-11
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 Score 1478;
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Query Match

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Sequence

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US-08-670-354-2
US-08-584-031-1
US-08-780-496-10
US-08-883-086-10
US-09-833-593A-6
US-09-333-593A-6
US-09-919-039-118
US-09-919-039-118
US-09-934-465-1
US-09-934-465-1
US-09-934-465-1
US-09-936-116-30
US-09-105-343A-7
US-09-105-343A-7
US-09-825-563-13
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US-09-825-563-13
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1478 1478 1469 1238 988 988 988 930 930 930 930 930

1478 1478

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Issued\_Patents\_AA:\*

1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*

2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*

3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*

4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*

5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*

6: /cgn2\_6/ptodata/1/iaa/backfIles1.pep:\*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Minimum DB Maximum DB

seq length: 0
seq length: 2000000000

Total number of hits satisfying chosen parameters:

513545 segs,

74649064 residues

Scoring table: Sequence: Perfect score:

BLOSUM62 Gapop 10.0 ,

Gapext 0.5

US-10-077-435-1 1478

1 MAMMEVQGGPSLGQTCVLIV.....NEHLIDMDHEASFFGAFLVG

2, 2005, 14:41:36; Search time 43 Seconds (without alignments) 487.823 Million cell updates/sec

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; Sequence 1, Application US/08584031A
Patent No. 6030945
; GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: APO-2 LIGAND
FILE REFERENCE: 11669.22US03
; CURRENT APPLICATION NUMBER: US/08/584,031A
; CURRENT FILING DATE: 1996-01-09
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
RESULT 3
US-08-780-496-1
; Sequence 1, Application US/08780496
; Patent No. 6046048
; GENERAL INFORMATION:
; APPLICANT: Avi Ashkenazi, Anan (
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; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-584-031-1
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Anan Chuntharapai, Kyung Jin
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                                                                                                                                              Sequence 10, Application US/08883086
Patent No. 6171787
GENERAL INFORMATION:
APPLICANT: WILEY, STEVEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; S
Best Local Similarity 100.0%; F
Matches 281; Conservative 0;
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: MATSCHANG, Diane L.
REGISTRATION UNMER: 35,600
REFERENCE/DOCKET NUMBER: P097
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-2416
TELEPAX: 415/952-9881
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ZIP: 94080
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                              TITLE OF INVENTION: MEMBER OF THE TITLE OF INVENTION: FOR TREATMENT NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSE: Abbott Laboratories
STREET: 100 Abbott Park Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: AF NUMBER OF SEQUENCES: ECORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 281 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/0 FILING DATE: 08-Jan-1997 CLASSIFICATION: 435
                 CITY: Abbott Park
STATE: IL
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Pred. No. 3.5e-149;
); Mismatches 0;
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                                                                                                                  FAMILY USEFUL
DIAGNOSIS OF 1
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CURRENT APPLICATION NUMBER: US/09/320,424
CURRENT FILING DATE: 1999-05-26
EARLIER APPLICATION NUMBER: 09/190,046
EARLIER FILING DATE: 1998-11-10
EARLIER APPLICATION NUMBER: 09/048,641
EARLIER FILING DATE: 1998-03-26
EARLIER FILING DATE: 1996-06-25
EARLIER FILING DATE: 1996-06-25
                                                                                                                               Sequence 2, Application US/09320424
Patent No. 6284236
GRMERAL INFORMATION:
APPLICANT: Wiley, Steven R.
APPLICANT: Goodwin, Raymond G.
TITLE OF INVENTION: Cytokine that Induces Apoptosis
FILE REFERENCE: 2835-E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 281; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: POTembski, Priscilla E.
REGISTRATION NUMBER: 3,207
REFERENCE/DOCKET NUMBER: 6134
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-937-0378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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TOPOLOGY: lir
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FILE REFERENCE: GH-50008-2
CURRENT APPLICATION NUMBER: US/09/333,593A
CURRENT FILING DATE: 1999-06-15
PRIOR APPLICATION NUMBER: 08/916,625
PRIOR APPLICATION NUMBER: 08/853,684
PRIOR FILING DATE: 1997-05-09
PRIOR FILING DATE: 1997-05-09
PRIOR APPLICATION NUMBER: 60/041,230
PRIOR APPLICATION NUMBER: 60/041,230
PRIOR FILING DATE: 1997-03-14
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 6
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; ORGANISM: human
US-09-320-424-2
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                               Query Match
Best Local S
Matches 281
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SEQ ID NO 2 .
LENGTH: 281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No.
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EARLIER FILING DATE: 1995-11-01
EARLIER FILING DATE: 1995-06-29
NUMBER OF SEQ ID NOS: 25
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: TRUNEH, ALEMSEGED TITLE OF INVENTION: TUMOR NETITLE OF INVENTION: TR6
                                                                                                                                      LENGTH: 281
TYPE: PRT
ORGANISM: HOMO SAPIENS
                                                                  Local Similarity
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MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
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YOUNG, PETER R.
MARSHALL, LISA A.
ROSHAK, AMY K.
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                                              100.0%; Score 1478; DB 3; ilarity 100.0%; Pred. No. 3.5e-149; Conservative 0; Mismatches 0;
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US-09-157-864-11
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                                                                                                                                                                                                                                                                               CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Ketber, Lori L.
REGISTRATION NUMBER: 41,113
REFERENCE/DOCKET NUMBER: 6111.N CN
TELEPHONE: 616/833-0974
TELEPHONE: 616/833-0974
TELEPAX: 616/833-8897
TELEPAX: 616/833-8897
TELEPX 224401
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
IENUTERISTICS:
                                                                                                                                             Query Match
Best Local Similarity
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                                                                                                                                Matches
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APPLICANT: Bienkowski, Michael J
APPLICANT: Mills, Cynthia J
APPLICANT: Jones, David A
TITLE OF INVENTION: TNF-Related Death Ligand
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/157,864
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MEDIUM TYPE: 3.5 Diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING TO THE T
                                                                                                                                                                                                                      STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                   TYPE: amino acids
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ADDRESSEE: Legal Services
STREET: 301 Henrietta Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241
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6440694
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                      DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ
                                                                 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
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Pred. No. 3.5e-149;
); Mismatches 0;
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RESULT 9
US-09-919-039-118
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Patent No. 652122
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CURRENT APPLICATION NUMBER: US/09/825,563
CURRENT FILING DATE: 2001-04-02
PRIOR APPLICATION NUMBER: 09/320,424
PRIOR FILING DATE: 1999-05-26
PRIOR PILING DATE: 1999-05-26
PRIOR FILING DATE: 1998-11-01
PRIOR APPLICATION NUMBER: 09/048,641
PRIOR APPLICATION NUMBER: 09/048,641
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 08/670,354
PRIOR FILING DATE: 1996-06-25
PRIOR APPLICATION NUMBER: 08/548,368
PRIOR APPLICATION NUMBER: 08/548,368
PRIOR APPLICATION NUMBER: 08/496,632
PRIOR APPLICATION NUMBER: 08/496,632
PRIOR FILING DATE: 1995-06-29
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATENTIN PATENTING DATE: 1995-06-29
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATENTIN PATENTING DATE: 1995-06-29
NUMBER OF SEQ ID NOS: 25
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APPLICANT: Goodwin, Raymond G.
TITLE OP INVENTION: Cytokine that Induces Apoptosis
FILE REFERENCE: 2835-E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 100.0%; S Local Similarity 100.0%; P Post 281; Conservative 0;
                                                                                                                                                                                                                                     121 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG
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Pred. No. 3.5e-149;
); Mismatches 0;
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March 18 . Se

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RESULT 10
US-09-582-450-1
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                                                                            US-09-582-450-1
                                                                                                                                                                                                                                                                                                   APPLICANT: Ashkenazi, Avi J.
APPLICANT: Kelley, Robert F.
APPLICANT: O'Connell, Mark P.
APPLICANT: Pitti, Robert M.
APPLICANT: Schwall, Ralph H.
TITLE OF INVENTION: Apo-2 Ligand
FILE REFERENCE: P0978P4
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TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES FILE REFERENCE: PA-0035 US
CURRENT APPLICATION NUMBER: US/09/919,039
CURRENT FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: 60/222,113
PRIOR APPLICATION NUMBER: 60/222,113
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 401
SOFTWARE: PERL Program
SEQ ID NO 118
LENGTH: 281
TYPE: DET
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/09582450 Patent No. 6740739
                                                                                                                                SEQ ID NO 1
LENGTH: 281
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Best Local Similarity
Query Match 100.0%; 9
Best Local Similarity 100.0%; 1
Matches 281; Conservative 0;
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                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/582,450 CURRENT FILING DATE: 2001-05-14 PRIOR APPLICATION NUMBER: US 09/007,886 PRIOR FILING DATE: 1998-01-15 PRIOR APPLICATION NUMBER: US 09/060,533 PRIOR FILING DATE: 1998-04-15
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                                                                                                                                                                      NUMBER OF SEQ ID NOS: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE: misc_feature
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No.
                                                                                           TYPE: PRT
ORGANISM: Homo
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Score 1478; DB 4;
Pred. No. 3.5e-149;
Mismatches 0;
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RESULT 12 US-10-011-125A-4

Sequence 4, Application US/10011125A Patent No. 6828121 GENERAL INFORMATION: APPLICANT: Chen, Christina Yu-Ching

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Sequence 1, Application US/09934465
Patent No. 6746668
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: APO-2 LIGAND
FILE REFERENCE: 11669.22US03
CURRENT APPLICATION NUMBER: US/09/934,465
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: 08/584,031
PRIOR APPLICATION NUMBER: 08/584,031
PRIOR FILING DATE: 1996-01-09
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 281
TYPE: PRT
ORGANISM: Homo sapiens
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US-09-934-465-1
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                                                                                                                     RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG
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FILE REFERENCE: P1804R1
CURRENT APPLICATION NUMBER: US/10/011,125A
CURRENT FILING DATE: 2001-12-07
PRIOR APPLICATION NUMBER: US 60/256,162
PRIOR FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 12
SEQ ID NO 4
LENGTH: 281
TYPE: PRT
ORGANISM: Homo sapiens
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PCT-US96-10895-2
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GENERAL INFORMATION:
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Best Local Similarity
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                CLASSIFICATION:
ATTORNEY JAGENT INFORMATION:
NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
                                                                                            FILING DATE: 29-JUN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/548,368
FILING DATE: 01-NOV-1995
                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.5.2
SOFTWARE: Microsoft Word, Version 6.0.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Immunex Corporation.
TITLE OF INVENTION: Cytokine That Induces Apoptosis
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/496,632
FILING DATE: 29-JUN-1995
                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 25-JUN CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 51 University Street CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
REFERENCE/DOCKET NUMBER:
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2835-WO
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CURRENT APPLICATION NUMBER: US/09/072,993C
CURRENT FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/05,513
PRIOR FILING DATE: 1997-08-13
PRIOR APPLICATION NUMBER: 60/056,980
PRIOR APPLICATION NUMBER: 60/056,980
PRIOR PILING DATE: 1997-08-26
PRIOR PILING DATE: 1997-08-26
PRIOR PILING DATE: 1997-08-29
NUMBER: 60/057,550
PRIOR PILING DATE: 1997-08-29
NUMBER: F8ST ID NOS: 9
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 3
LENGTH: 279
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US96-10895-2
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                                                                                                                                                                                                                             US-09-072-993C-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/09072993C
Patent No. 6346388
GENERAL INFORMATION:
APPLICANT: Michael R. Brigham-Burke
APPLICANT: Peter R. Young
TITLE OF INVENTION: ANTAGONIST FOR TUMOR NECROSIS RELATED RECEPTORS TR1 AND
TITLE OF INVENTION: ANTAGONISTS FOR TUMOR NECROSIS RELATED RECEPTORS TR1 AND TR2
FILE REFERENCE: GH-50030
                                                                                                                                  Query Match
Best Local Similarity
Matches 279; Conserv
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Best Local Similarity 100.0%;
Matches 281; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                LENGTH: 27
TYPE: PRT
                                                                                                                                                                                                                                                ORGANISM: HOMO SAPIENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241
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SYMDPNDEESMNSPCWQVKWQLRQLVRKM1LRTSEET1STVQEKQQNISPLVRERGPQRV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240
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                                                                MMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKEDD
                                                                                                       MEVOGGPSLGOTCVLIVIFTVLLOSLCVAVTYVYFTNELKOMODKYSKSGIACFLKEDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ
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                                                                                                                                            99.4%; Score 1469; DB 3; I ilarity 100.0%; Pred. No. 3.1e-148; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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Pred. No. 3.5e-149;
0; Mismatches 0;
                                                                                                                                                                                      Length 279;
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| Search completed: March 2, 2005, 14:52:32<br>Job time : 52 secs | Qy 181 FYYIYSQTYFREQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY | Qy 61 DDSYMDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ                             | Best Local Similarity 85.4%; Pred. No. 1.3e-123; Best Local Similarity 85.4%; Pred. No. 1.3e-123; Matches 240; Conservative 2; Mismatches 5; Indels 34; Gaps  Matches 240; Conservative 2; Mismatches 5; Indels 34; Gaps  Oy 1 MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE | RESULT 15 US-09-569-611C-30 US-09-569-611C-30 US-09-569-611C-30 IS Sequence 30, Application US/09569611C Patent No. 6720182 GENERAL INFORMATION: APPLICANT: SAVITZKY et al. TITLE OF INVENTION: ALTERNATIVE SPLICING VARIANTS FILE REFERENCE: 2786-0151P CURRENT APPLICATION NUMBER: US/09/569,611C CURRENT FILING DATE: 2000-05-10 INUMBER OF SEQ ID NOS: 52 SOFTWARE: Patentin Ver. 2.0 IENGTH: 271 TYPE: PRT ORGANISM: Homo sapiens US-09-569-611C-30 | Db 181 YIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPIL  Qy 243 YQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG | 123<br>121<br>183 | Db 61 SYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQRV |
|---|---|--|---|--|--|-------------------|--|
|   | DPILLMKSARNSCWSKDAEYGLY 240   | ETISTVQEKQQNISPLVRERGPQ 120 :                KSNKIFLPLVRERGPQ 130 :RSGHSFLSNLHLRNGELVIHEKG 180 | 5; Indels 34; Gaps 2; FTNELKOMODKYSKSGIACFLKE 60  | δ  | ILLMKSARNSCWSKDAEYGLYSI 240<br>NG 281<br>  |                   | ISTVQEKQQNISPLVRERGPQRV 120  |

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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                              seq length: 0 seq length: 2000000000
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1: /cgn2_6/ptodata/2/pubpaa/US07 PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/US06 NEW PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US06 NEW PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US07 NEW PUB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/US07 NEW PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/US07 NEW PUB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/US08 NEW PUB.pep:*

9: /cgn2_6/ptodata/2/pubpaa/US08 NEW PUB.pep:*

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10: /cgn2_6/ptodata/2/pubpaa/US09 PUBCOMB.pep:*

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12: /cgn2_6/ptodata/2/pubpaa/US09 PUBCOMB.pep:*

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Match Length DB
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Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                US-08-916-625B-6
US-08-971-317A-8
US-09-813-329-17
US-09-193-663-8
US-09-934-465-1
US-09-919-039-118
3 US-10-011-125-4
4 US-10-003-766-4-94
4 US-10-003-766-4-11
4 US-10-174-654-11
5 US-10-174-654-11
5 US-10-174-654-11
6 US-10-185-882-41
6 US-10-322-673-72
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Sequence 6, Appli
Sequence 8, Appli
Sequence 17, Appl
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 4, Appli
Sequence 54, Appl
Sequence 54, Appl
Sequence 11, Appl
Sequence 41, Appl
Sequence 20, Appl
Sequence 72, Appl
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|-------------------|-------------------|-------|----------|-----------------|-----------------|-------------------|----------|------------------|----------|------------------|------------------|------------------|-------------------|-------------------|------------------|--------------|-----------|-----------|----------|----------|-----------------|-----------------|--------------|------|-------------------|--------------|-----------------|-----------------|-----------------|------------------|-------------------|
| 887               | 890               | 892.5 | 930      | 930             | 930             | 937.5             | 964.5    | 978              | 982      | 985.5            | 988              | 988              | 1017              | 1269.5            | 1456             | 1469         | 1478      | 1478      | J        | 1478     | 1478            | 1478            | 1478         | 1478 | 1478              | 1478         | 1478            | 1478            | 1478            | 1478             | 1478              |
| 60.0              | 60.2              | 60.4  | 62.9     | 62.9            | 62.9            | 63.4              | 65.3     | 66.2             | 66.4     | 66.7             | 66.8             | 66.8             | 68.8              | 85.9              | 98.5             | •            | •         | 100.0     | 100.0    | 100.0    | 100.0           | 100.0           | •            | •    | 100.0             | •            | •               |                 | .0              | 100.0            | 100.0             |
| 168               | 287               | 228   | 291      | 291             | 291             | 188               | 296      | 614              | 480      | 461              | 256              | 253              | 208               | 246               | 279              | 279          | 281       | 281       | 281      | 281      | 281             | 281             | 281          | 281  | 281               | 281          | 281             | 281             | 281             | 281              | 281               |
| 9                 | 16                | 17    | 15       | 13              | 10              | 9                 | 14       | 15               | 15       | 15               | 15               | 15               | 9                 | 9                 | 16               | 13           | 17        | 17        |          | 16       | 16              | 15              |              | 15   | 15                |              | 15              |                 | 15              | 14               | 14                |
| US-09-900-530A-10 | US-10-367-094-15  | -10-  | -10-652- | US-10-017-910-6 | US-09-873-829-6 | US-09-855-544A-14 | -10-185- | US-10-389-223A-2 | -10-389- | US-10-389-223A-6 | US-10-652-244-13 | US-10-652-244-11 | US-09-855-544A-16 | US-09-855-544A-13 | US-10-367-094-22 | -10-066-209- | -10-855-5 | -10-771-2 | -10-491- | -10-755- | US-10-381-160-5 | US-10-652-244-2 | -10-662-430- | ٥    | 1                 | -10-662-429- | US-10-333-712-1 | US-10-292-486-5 | US-10-279-687-8 | US-10-310-793-26 | US-10-139-785-66  |
| 10, App           | Sequence 15, Appl | 4     | e<br>6,  | e 6, Appl       | e<br>6,         | 14,               | e<br>5,  | Ŋ                | e 4,     | ς,               | 13,              | e 11,            | 16,               | 13,               | 22,              | e 3,         | e 2, App  | ۲,        | 1, App   | e 210    | 5               | ν,              | 2            | ν,   | Sequence 20, Appl | e 2,         | e<br>1,         | e 5,            | е 8, 2          | e 26,            | Sequence 66, Appl |

## ALIGNMENTS

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US-08-916-625B-6

; Sequence 6, Application US/08916625B

; Sequence 6, Application US/08916625B

; Publication No. US20010010924A1

GENERAL INFORMATION:

APPLICANT: DEEN, KEITH C.

APPLICANT: YOUNG, PETER R.

ITILE OF INVENTION: TUMOR NECROSIS FACTOR RELATED

TITLE OF INVENTION: RECEPTOR, TR6

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSE: RAINER & PRESTIA

STREET: P.O. BOX 980

CITY: VALLEY FORGE

STATE: PA

COUNTRY: USA
ZIP: 19482

COMPUTER READABLE FORM:

MEDDIUM TYPE: Diskette

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

OPERATION SYSTEM: DOS

SOFTWARE: FASTESQ for Windows Version 2.0

CURRENT APPLICATION DATTA:

APPLICATION NUMBER: US/08/916,625B

FILING DATE: 22-AUG-1997

APPLICATION NUMBER: 08/853,684

FILING DATE: 09-MAY-1997

APPLICATION NUMBER: 60/041,230

FILING DATE: 14-MARCH-1997

ATTORNEY/AGENT INFORMATION:

NAME: PRESTIA, PAUL F

REGISTRATION NUMBER: 63.031

REFERENCE/DOCKET NUMBER: GH-50008-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 8, Application US/08971317A
Publication No. US20010010925A1
GENERAL INFORMATION:
APPLICANT: Wiley, Steven R.
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                                                                                                                                                          ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/971,317A
FILING DATE: 17-NOV-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
NAME: GOller, Mimi C
REGISTRATION UNMBER: 39,046
REFERENCE/DOCKET NUMBER: 6255
TELECOMMUNICATION INFORMATION:
TELEPHONE: (847) 935-7550
TELEPAX: (847) 938-2623
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CORRESPONDENCE ADDRESS:
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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                            FILING DATE:
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TELEFAX: 610-407-0701
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1.2e-128;
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Patent No. US20020012968A1

APPLICANT: Bristol-Myers Suibb Company
TITLE OF INVENTION: No. US20020012968A1e1 Drosophila Tumor Necrosis Factor Class Mole
TITLE OF INVENTION: Variants Thereof
FILE REFERENCE: D0016.np
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                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 65
SOFTWARE: PatentIn version 3.0
SEQ ID NO 17
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CURRENT FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: 60/190,816
PRIOR FILING DATE: 2000-03-21
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SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
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TOPOLOGY: linear
MOLECULE TYPE: No. US20010010925A1e
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FYYIYSQTYFREQEEIKENTKNDKQMVQXIYKYTSYPDFILLMKSARNSCWSKDAEYGLY
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APPLICANT: Wiley, Steven R.

TITLE OF INVENTION: TWP-DELTA LIGAND AND USES THEREOF
FILE REFERENCE: 6255 US.02
CURRENT APPLICATION NUMBER: US/09/193,663
CURRENT FILING DATE: 1998-11-17
EARLIER APPLICATION NUMBER: 60/065,916
EARLIER FILING DATE: 1997-11-17
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 8
LENGTH: 281
                                   Requence 1, Application US/0934465
PATENT NO. US20020102233A1

GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: APO-2 LIGAND
FILE REFERENCE: 11669.22953
CURRENT APPLICATION NUMBER: US/09/934,465
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: 08/584,031
PRIOR APPLICATION NUMBER: 08/584,031
PRIOR APPLICATION PRIOR OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 281
TYPE: PRT
ORGANISM: Homo sapiens
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US-09-934-465-1
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Best Local Similarity
Query Match
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ORGANISM: Homo sapiens
-09-193-663-8
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Pred. No. 1.2e-128;
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 Score 1478;
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; FEATURE:
; NAME/KBY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030108871A1 059509CD1
US-09-919-039-118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PERL Program
SEQ ID NO 118
LENGTH: 281
TYPE: PRT
ORGANISM: Homo Bapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES FILE REFERENCE: PA-0.035 US
CURRENT APPLICATION NUMBER: US/09/919,039
CURRENT FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: 60/222,113
PRIOR APPLICATION NUMBER: 60/222,113
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 401
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SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG
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o. US20030108871A1
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Pred. No. 1.2e-128;
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DATE:

60/085149

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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Chen, Christina Yu-Ching

TITLE OF INVENTION: BACTERIAL HOST STRAINS

FILE REFERENCE: P1804R1

CURRENT APPLICATION NUMBER: US/10/011,125

CURRENT FILING DATE: 2001-12-07

PRIOR APPLICATION NUMBER: US 60/256,162

PRIOR FILING DATE: 2000-12-14

NUMBER OF SEQ ID NOS: 10

SEQ ID NO 4

LENGTH: 281

TYPE: PRT

ORGANISM: Homo sapiens

US-10-011-125-4
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 54, ... Sequence 54, ... 182004; Publication No. US2004; Publication No. US2004; Publication No. US2004
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US-10-001-054-54
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              PRIOR APPLICATION NUMBER: 60/059114
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079920
PRIOR FILING DATE: 1998-03-30
PRIOR FILING DATE: 1998-03-30
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/082999
PRIOR FILING DATE: 1998-04-24
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Publication No. US20020142388A1
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Best Local (
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APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin
APPLICANT: Wood, William
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC
TITLE OF INVENTION: CELL GROWTH
                                                                                                                                                              FILE REFERENCE: P3034R1PCT
CURRENT APPLICATION NUMBER: US/10/001,054
CURRENT FILING DATE: 2001-11-30
 APPLICATION NUMBER: 60/082999
FILING DATE: 1998-04-24
APPLICATION NUMBER: 60/083545
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Goddard, Audrey
Gurney, Austin
Hebert, Carolyn
Henzel, William
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No. US20020192209A1
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OR APPLICATION NUMBER: 60/232887
OR APPLICATION NUMBER: 60/232887
OR APPLICATION NUMBER: 09/180997
OR FILING DATE: 1998-11-19
OR APPLICATION NUMBER: 09/18517
OR APPLICATION NUMBER: 09/284291
OR APPLICATION NUMBER: 09/284291
OR FILING DATE: 1999-04-12
OR FILING DATE: 1999-04-12
                                                    DR FILING DATE: 1999-08-25
OR APPLICATION NUMBER: 09/380913
OR FILING DATE: 1999-09-09
OR APPLICATION NUMBER: 09/403297
OR FILING DATE: 1999-10-18
OR APPLICATION NUMBER: 09/423741
                                                                                                                                                                                                                                                                                                                                                                                                               DR APPLICATION NUMBER: 60/144758
DR FILING DATE: 1999-07-20
DR APPLICATION NUMBER: 60/162506
DR FILING DATE: 1999-10-29
DR APPLICATION NUMBER: 60/170262
DR FILING DATE: 1999-12-09
DR APPLICATION NUMBER: 60/187202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OR FILING DATE: 1999-03-10
PRINCATION NUMBER: 60/131294
OR FILING DATE: 1999-04-07
OR APPLICATION NUMBER: 60/140650
OR FILING DATE: 1999-06-22
OR APPLICATION NUMBER: 60/141037
OR APPLICATION NUMBER: 60/141037
OR APPLICATION NUMBER: 60/141037
OR FILING DATE: 1999-06-23
APPLICATION NI FILING DATE:
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FILING DATE: 1999-01-20
APPLICATION NUMBER: 60/123618
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FILING DATE: 1998-12-15
APPLICATION NUMBER: 60/113296
FILING DATE: 1998-12-22
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APPLICATION NUMBER: 60/108849
FILING DATE: 1998-11-18
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FILING DATE: 1998-06-02
APPLICATION NUMBER: 60/088858
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FILING DATE: 1998-05-12
                                                                                                                                                               APPLICATION NUMBER: 09/380138
                                                                                                                                                                              APPLICATION NUMBER: 09/380137
FILING DATE: 1999-08-25
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FILING DATE: 1999-01-12
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60/115554

1999-11-10

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PRIOR
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OR FILING DATE: 2000-03-30
OR APPLICATION NUMBER: PCT/US00/13705
OR FILING DATE: 2000-05-17
OR APPLICATION NUMBER: PCT/US00/14042
OR APPLICATION NUMBER: PCT/US00/14042
OR FILING DATE: 2000-05-22
                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 2000-02-18
APPLICATION NUMBER: PCT/US00/04342
FILING DATE: 2000-02-18
APPLICATION NUMBER: PCT/US00/05841
FILING DATE: 2000-03-02
APPLICATION NUMBER: PCT/US00/06884
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APPLICATION NUMBER: 09/918585
FILING DATE: 2001-07-30
                                                                                FILING DATE: 2000-06-02
APPLICATION NUMBER: PCT/US00/22031
FILING DATE: 2000-08-11
APPLICATION NUMBER: PCT/US00/23522
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APPLICATION NUMBER: PCT/US99/12252
FILING DATE: 1999-06-02
APPLICATION NUMBER: PCT/US99/20111
FILING DATE: 1999-09-01
APPLICATION NUMBER: PCT/US99/20594
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APPLICATION NUMBER: 09/882636
                                                                                                                                              APPLICATION NUMBER: PCT/US00/15264
FILING DATE: 2000-06-02
                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/US00/14941
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APPLICATION NUMBER: PCT/US99/28551
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/US98/18824 FILING DATE: 1998-09-10
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FILING DATE: 2001-08-28
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FILING DATE: 2001-05-25
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FILING DATE: 2001-03-09
                    APPLICATION NUMBER: PCT/US00/30873 FILING DATE: 2000-11-10
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FILING DATE: 2000-02-11
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FILING DATE: 1999-11-30
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PCT/US00/32678
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; NUMBER OF SEQ ID
; SEQ ID NO 54
; LENGTH: 281
; TYPE: PRT
; ORGANISM: HOMO S
US-10-001-054-54
Sequence 54, Application US/10093766
Publication No. US20030013099A1
GENERAL INFORMATION:
APPLICANT: Lasek, Amy W.
APPLICANT: Lasek, Amy W.
APPLICANT: Lasek, David A.
APPLICANT: Karpf, Adam R.
TITLE OF INVENTION: GENES REGULATED BY DNA MET FILE REFERENCE: PA-0047 US
CURRENT FLILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PERL PROGram
SEQ ID NO 54
LENGTH: 281
TYPE: PRT
TYPE: PRT
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US-10-093-766-54
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PRIOR APPLICATION NUMBER: PCT/USO1/06520
PRIOR APPLICATION NUMBER: PCT/USO1/06666
PRIOR APPLICATION NUMBER: PCT/USO1/106666
PRIOR APPLICATION NUMBER: PCT/USO1/17092
PRIOR FILING DATE: 2001-05-25
PRIOR PILING DATE: 2001-06-25
PRIOR PILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: PCT/USO1/17800
PRIOR APPLICATION NUMBER: PCT/USO1/19692
PRIOR FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: PCT/USO1/21066
PRIOR PRIOR APPLICATION NUMBER: PCT/USO1/21066
PRIOR APPLICATION NUMBER: PCT/USO1/21735
PRIOR APPLICATION NUMBER: PCT/USO1/27099
PRIOR APPLICATION NUMBER: PCT/USO1/27099
PRIOR FILING DATE: 2001-07-09
PRIOR PILING DATE: 2001-07-09
PRIOR PILING DATE: 2001-08-29
PRIOR FILING DATE: 2001-08-29
PRIOR FILING DATE: 2001-08-29
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Best Local Similarity
Matches 281; Conserv
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milarity 100.0%;
Conservative 0;
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Pred. No. 1.2e-128;
); Mismatches 0;
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120

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US-10-093-766-54
Query Match
                                      FEATURE: misc feat NAME/KEY: misc feat OTHER INFORMATION:
                                                   feature
                                        Incyte ID
100.0%;
                                        No. US20030013099A1 059509CD1
 Score 1478;
 멺
 14;
Length 281;
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240 180 180 120 120 60

240

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EQUENCE DESCRIPTION: SEQ ID NO: US-10-174-654-11
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US-10-174-654-11
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               Query Match
Best Local Similarity
Matches 281; Conserv
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                                                                                                                                                                                                                                             INFORMATION
                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 Diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION NUMBER: US/10/174,654
FILING DATE: 19-Jun-2002
CLASSIFICATION: CUNCHOWND
ATTORNEY/AGENT INFORMATION:
NAME: Kerber, Lori L.
REGISTRATION NUMBER: 41,113
REFERENCE/DOCKET NUMBER: 6111.N CN1
TELEPHONE: 616/833-0974
TELEPHONE: 616/833-8897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mills, Cynthia J
Jones, David A
TITLE OF INVENTION: TNF-Related Death Ligand
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                  TELEX: 224401
WATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
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STREET: 301 Henrietta Street
CITY: Kalamazoo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 49001
                                                                                                                              TOPOLOGY: linear
                                                                                                                                                                                LENGTH: 281 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: MI
                                                                                                                                                               STRANDEDNESS: single
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                     Conservative
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                 100.0%; Score 1478;
100.0%; Pred. No. 1.2
cive 0; Mismatches
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                                  1.2e-128;
                                                     DB 14;
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US-10-151-882-41
US-10-151-882-41
; Sequence 41, Application US/10151882
; Publication No. US20030059862A1
; GENERAL INFORMATION:
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               Sequence 20, Application US/10218547
Publication No. US20030100074A1
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, II
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Best Local Similarity
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TITLE OF INVENTION: Antibodies Against Tumor
FILE REFERENCE: PF554
CURRENT APPLICATION NUMBER: US/10/151,882
CURRENT FILING DATE: 2002-05-22
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ORGANISM: Homo
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CANT: Human Genome Sciences, Inc. OF INVENTION: Methods And Compositions
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FILE REFERENCE: PF561
CURRENT APPLICATION NUMBER: US/10/218,547
CURRENT FILING DATE: 2002-08-15
PRIOR APPLICATION NUMBER: 60/312,542
PRIOR FILING DATE: 2001-08-16
PRIOR APPLICATION NUMBER: 60/330,761
PRIOR APPLICATION NUMBER: 60/330,761
PRIOR FILING DATE: 2001-10-30
NUMBER OF SEQ ID NOS: 57
SOFTWARE: Patentin version 3.1
SEQ ID NO 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 13
US-10-322-673-72
; Sequence 72, Application US/10322673
; Publication No. US20030180296A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: PF585
                                                                 PRIOR APPLICATION NUMBER: 60/425,737
PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 72
; SEQ ID NO 72
; SEQ ID NO 72
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-322-673-72
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CURRENT FILING DATE: 2002-12-19
PRIOR APPLICATION NUMBER: 60/341,237
PRIOR FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: 60/369,877
PRIOR TILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: 60/384,828
PRIOR APPLICATION NUMBER: 60/384,828
PRIOR FILING DATE: 2002-06-04
PRIOR APPLICATION NUMBER: 60/396,591
PRIOR APPLICATION NUMBER: 60/403,370
PRIOR APPLICATION NUMBER: 60/403,370
PRIOR APPLICATION NUMBER: 60/403,370
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TYPE: PRT
ORGANISM: human
S-10-218-547-20
Query Match
Best Local Similarity
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                                                                                                                                                                                                                                         2002-08-15
        100.0%;
        Score 1478; DB 14; Pred. No. 1.2e-128;
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-139-785-66
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PRIOR PILLING DATE: 2002-04-05
PRIOR PILLING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: 60/341,237
PRIOR PILLING DATE: 2001-11-14
PRIOR PILLING DATE: 2001-11-14
PRIOR PPLICATION NUMBER: 60/331,310
PRIOR PPLICATION NUMBER: 60/331,044
PRIOR PILLING DATE: 2001-11-07
PRIOR PILLING DATE: 2001-11-07
PRIOR APPLICATION NUMBER: 60/327,364
PRIOR PILLING DATE: 2001-09-21
PRIOR PILLING DATE: 2001-09-21
PRIOR PILLING DATE: 2001-09-21
PRIOR APPLICATION NUMBER: 60/323,807
PRIOR PILLING DATE: 2001-09-21
PRIOR APPLICATION NUMBER: 60/399,176
PRIOR APPLICATION NUMBER: 60/294,981
PRIOR PILLING DATE: 2001-06-04
PRIOR PILLING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: 60/294,981
PRIOR APPLICATION NUMBER: 60/293,473
PRIOR FILLING DATE: 2001-06-04
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SEQ ID NO 66
LENGTH: 281
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CURRENT APPLICATION NUMBER: US/10/139,785
CURRENT FILING DATE: 2002-05-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TITLE OF INVENTION: Receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Salcedo et al.
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RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG 180
                                                               DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ
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                                                                                                                                                                                           MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKE
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                                                                                                                                                                                                                                                                                                                    100.0%; Score 1478; DB 14; llarity 100.0%; Pred. No. 1.2e-128; Conservative 0; Mismatches 0;
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PRIOR APPLICATION NUMBER: 60/336,695
PRIOR FILING DATE: 2002-12-07
PRIOR FILING DATE: 2001-12-07
PRIOR PELLING DATE: 2001-12-07
PRIOR FILING DATE: 2001-12-07
PRIOR FILING DATE: 2001-08-23
PRIOR APPLICATION NUMBER: 60/314,381
PRIOR FILING DATE: 2001-08-24
PRIOR FILING DATE: 2001-08-24
PRIOR PPLICATION NUMBER: 09/899,059
PRIOR PPLICATION NUMBER: 09/278,449
PRIOR PILLING DATE: 2001-03-26
PRIOR PILLING DATE: 2001-03-26
PRIOR PILLING DATE: 2000-07-07
PRIOR PILLING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: 60/216,879
PRIOR APPLICATION NUMBER: 60/180,908
PRIOR APPLICATION NUMBER: 60/180,908
PRIOR APPLICATION NUMBER: 60/134,067
PRIOR PILLING DATE: 2000-02-08
PRIOR PILLING DATE: 2000-05-13
PRIOR PILLING DATE: 1999-05-13
PRIOR APPLICATION NUMBER: 60/134,067
PRIOR PILLING DATE: 1999-05-13
PRIOR PRIOR APPLICATION NUMBER: 60/132,227
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SEQ ID NO 26
LENGTH: 281
TYPE: PRT
ORGANISM: human
S-10-310-793-26
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Best Local Similarity
Matches 281; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/134,067
PRIOR FILING DATE: 1999-05-13
PRIOR APPLICATION NUMBER: 60/132,227
PRIOR FILING DATE: 1999-05-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Methods And Compositions For Treating Inflammatory Bowel Diseases TITLE OF INVENTION: Relating To Human Tumor Necrosis Factor-Gamma Beta FILE REFERENCE: PF573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Remaining Prior Application data removed - See File Wrapper or PALM.
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Db 181 FYYIYSQTYPRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY 240

QY 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

Db 241 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 281

Search completed: March 2, 2005, 15:03:07 Job time: 144 secs

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submitted to the EMBL Data
submitted number: S57565
                                                                                                   R;Suda, T.; Takahashi, T.; Golstein, P.; Nagata, S. Cell 75, 1169-1178, 1993
A;Title: Molecular cloning and expression of the Fas ligand, A;Reference number: A49266; MUID:94084792; PMID:7505205
A;Accession: A49266
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C;Keywords: glycoprotein; transmembrane protein
F;80-102/Domain: transmembrane #status predicted •
F;76,184,250,260/Binding site: carbohydrate (Asn)
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A;Title: Fas ligand mediates activation-induced cell death A;Reference number: 138554; MUID:95105731; PMID:7528780
A;Accession: 138554
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A;Title: Role of Fas ligand in apoptosis induced by hepatitis C virus i A;Reference number: JC2340; MUID:95071350; PMID:7980502
A;Recession: JC2340
  C; Keywords:
                                    A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-278 <SUD>
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C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: A49266
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A; Residues: 1-281 < MIT>
                 A;Cross-references: UNIPROT:P36940; GB:U03470; NID:g440178;
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A; Molecule type: mRNA
A; Residues: 1-261 < MER>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Bos primigenius taurus
C;Date: 08-Jul-1995 #sequence_revi
C;Accession: S53090
                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:P51749; EMBL:Z48469; NID:g732569; PIDN:CAA88363.1; PID:g7325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary
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Matches 50
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LYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFG
                                                                                                                                                                                VAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSN--LHLRNG-ELVIHE 178
                                                                                                                                                                                                                                                     YWDPNDEESMNS--PCWQVKWQLRQLVRKWILRTSEETISTVQEKQQNISPLVRERGPQR 121
                                                                                                                                                                                                                                                                                                                          VQGGPSLGQTCVLIVIFTVLL--QSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKEDDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ISTVQEKQQNISPLVRERGPQRVAAHITGT-RGRSNTLSSPNSKNEKALGRKINSWESSR 158
                                                                         QGFYYIYTQVTFCSNRE---
                                                                                                          KGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYG
                                                                                                                                                                                                                   IQRCNKGEGSLSLLNCEEIRSRFEDLV-KDIMQNKE-----VKKKEKNFEMHKGDQEPQ-
                                                                                                                                                                                                                                                                                           VATGPPVSMK-IFMYLLTVFLITOMIGSALFAVYLHRRLDKIEDERNLHEDFVFMK---T
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                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                              ----ISEASSKTTSVL-----QW--APKGYYTLSNNLVTLENGKQLAVKR
                                                                                                                                                                                                                                                                                                                                                                                 11.1%;
25.9%;
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                                                                                                                                                                                                                                                                                                                                                                52;
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                                                                                                                                                                                                                                                                                                                                                                                 Score 164; DB 2;
Pred. No. 2.3e-06;
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                                                                         -TLSQAPFIASLCLKSPSGSERILLRAANTHSSSKPC--G
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CD40 ligand - human

CD40 ligand - human

N;Alternate names: glycoprotein 39; hCD40-L protein; T-cell antigen gp39; Ti
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence revision 02-Jul-1996 #text\_change 09-Jul-2004
C;Date: 02-Jul-1996; S28017; JH0793; S26694; S28852; I53476; S25684; S30593
C;Accession: S28017; JH0793; S26694; S28852; I53476; S25684; S30593
R;Hollenbaugh, D.; Grosmaire, L.S.; Kullas, C.D.; Chalupny, N.J.; Braesch-A

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R;Hollenbaugh, D.; varvener R;Hollenbaugh, D.; varvener EMBO J. 11, 4313-4321, 1992 EMBO J. The human T cell as

antigen gp39, a member of the

TNF gene

family,

18 a

ligand

Braesch-Andersen,

'n for

TRAP

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A;Molecule type: mRNA
A;Residues: 1-261 <SPR>
A;Residues: 1-261 <SPR>
A;Residues: GB:X67878; NID:938411; PIDN:CAA48077.1; PID:938412
A;Experimental source: peripheral blood T-cell
A;Experimental source: peripheral blood T-cell
A;Experimental source: peripheral blood T-cell
A;Experimental source: Mages, H.W.; Senger, G.; Kroczek, R.A.
Eur. J. Immunol. 22, 3191-3194, 1992
Eur. J. Immunol. 22, 3191-3194, 1992
A;Title: Cloning of TRAP, a ligand for CD40 on human T cells.
A;Reference number: S26694; MUID:93076854; PMID:1280226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:X68550; NID:g37269; PIDN:CAA48554.1; PID:g37270 R;Gauchat, J.F.; Aubry, J.P.; Mazzei, G.; Life, P.; Jomotte, T.; Elson, G FEBS Lett. 315, 259-266, 1993 A;Title: Human CD40-ligand: molecular cloning, cellular distribution and A;Reference number: S28852; MUID:93138085; PMID:7678552
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A;Title: Recombinant human CD40 ligand stimulates B cell proliferation and immunoglobul A;Reference number: JH0793; MUID:93094757; PMID:1281209
A;Accession: JH0793
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A; Accession: S28017
A; Molecule type: mRNA
tumor necrosis factor alpha precursor - rabbit N,Alternate names: cachectin; TNF alpha C;Species: Oryctolagus cuniculus (domestic rabbit) C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 C;Accession: A25454; A25451; \overline{JS0727}
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A;Cross-references: GDB:120632; OMIM:308230
A;Map position: Xq26-Xq26
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A;Residues: 1-261 <GAU>
A;Cross-references: EMBL:L07414;
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A;Molecule type: mRNA
A;Residues: 1-261 <GRA>
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                                                                                                                             A25451
                                                                                                                                                       RESULT
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;Spriggs, M.K.; Armitage, R.J.; Strockbine, L.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17 VLIVIFTVLL--OSLCVAVTYVYFTNELKOMODKYSKSGIACFLKEDDSYWDP----ND
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                                                                                                                                                                                                                                GQQSIHLGGVFELQPGASVFVNVTDPSQVSHGTGFTSFG
                                                                                                                                                                                                                                                                          GLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFG
                                                                                                                                                                                                                                                                                                                              AQVTFCSNREASSQAPFIASLCLKSPGRFER-----ILLRAANTHSSAKPC--
                                                                                                                                                                                                                                                                                                                                                                               SQTYFRFQEEIKENT-----KNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                 -Qw--AEKGYYTMSNNLVTLENGKQLTVKRQGLYYIY
                          10-Sep-1999
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                       #text_change
                                                                                                                                                                                                                                257
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i., Sato, T.
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C;Superfamily: tumor necrosis factor C;Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; F;1-81/Domain: propeptide #status predicted <PRO> F;82-234/Product: tumor necrosis factor #status predicted <MAT> F;19,20/Binding site: myristate (Lys) (covalent) #status predicted F;83/Binding site: carbohydrate (Ser) (covalent) #status predicted F;81/20/Binding site: carbohydrate (Ser) (covalent) #status predicted F;147-178/Disulfide bonds: #status predicted
R;Armitage, R.J.; Fanslow, W.C.; Strockbine, L.; Sato, T.; Cosman, D.; Spriggs, M.K.

Nature 357, 80-82, 1992
A;Title: Molecular and biological characterization of a A;Reference number: S21738; MUID:92244364; PMID:1374165
A;Accession: S21738
                                                                                                                              C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1993 #sequence_revision
C;Accession: $21738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Note: this sequence differs from that shown in having R;Shakhov, A.N.; Kuprash, D.V.; Azizov, M.M.; Jongeneel, Gene 95, 215-221, 1926 Gene 95, 215-221, 1926 A;Title: Structural analysis of the rabbit TNF locus, col A;Reference number: JH0309; MUID:91065534; PMID:2249779 A;Accession: JS0727
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Cross-references: GB:M60340;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-62,'Q',63-234 <SHA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: nucleic acid sequence not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-234 <IT2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: UNIPROT:P04924; GB:M12845; NID:g165759; PIDN:AAA31486.1; PID:g165760 R;Ito, H.; Shirai, T.; Yamamoto, S.; Akira, M.; Kawahara, S.; Todd, C.W.; Wallace, R.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1'-234 <ITO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Title: Molecular cloning and expression in Escherichia A; Reference number: A25454; MUID:86219711; PMID:3519137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Ito, H.; Yamamoto, S.; Kuroda, DNA 5, 149-156, 1986
                                                                                                                                                                                                      CD40 ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5, 157-165, 1986
                                                                                                                                                                                                                                                                                                                                                                241
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                                                                                                                                                                                                           - mouse
                                                                                                                                                                                                                                                                                                                                                           SIYQGGIFELKENDRIFVSVTNEHLIDMDHEAS-FFG 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VA-----NPQVEGQL-----QWLSQRANALLANGMKLTDNQLVVPADGLYLIYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QEEESPNN-----LHLVNPVAQMVTLRSASRALSD-----KPL------AHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NDEESMNSPCWQVKWQLRQLVRKMI-LRTSEETISTVQEKQQNISPLVRERGPQRVAAHI 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGPQGSKRCLCLSLFSFLL----VAGATTLF---
                                                                                                                                                                                                                                                                                                                    PIYLGGVFQLEKGDRLSTEVNQPEYLDLAESGQVYFG
                                                                                                                                                                                                                                                                                                                                                                                                          QVLFSGQ--
                                                                                                                                                                                                                                                                                                                                                                                                                                                    QTYFRFQEEIKENTKNDKQMVQYIYKY-TSYPDPILLMKSARNSCWSKDAEYG-----LY 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFYYIYS 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKEDDSYWDP
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                                                                                                                                                                                                                                                                                                                                                                                                          GCRSYVLLTHTVSRFAVSYPNKVNLLSAIKSPCHRETPEEAEPMAWYB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 141; DB 1;
Pred. No. 0.00017;
1; Mismatches 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      shown;
                                                                                                                                                          31-Dec-1993 #text_change 09-Jul-2004
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                                                                                                             T.A.;
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, C.V.; Nedospasov,
                                                   murine
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                                                                                                                  Clifford,
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                                                                                                                  K.N.; Macduff,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PID:g165756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               macrophage;
                                                     CD40
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A;Residues: 1-260 <ARM>
A;Ross-references: UNIPROT: P27548; EMBL: X65453; NID:g50351; PIDN: CAA46448.1; PID:g50352
C;Keywords: glycoprotein; transmembrane protein
F;23-46/Domain: transmembrane #status predicted <TMM>
F;47-260/Domain: extracellular #status predicted <EXT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tumor necrosis factor beta precursor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change
C;Accession: S17289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: UNIPROT:P26445; EMBL:X54859; NID:g2132; PIDN:CAA38638.1; PID:g2133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Title: The porcine tumor necrosis factor-encoding genes: A;Reference number: S17289; MUID:91340150; PMID:1874444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Residues: 1-204 < KUH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
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                                                                                            SFFGAF 278
                                                                                                                                                                                                             TS-YPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEA 272
                                                                                                                                                                                                                                                                                                                               WESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKY
                                                                                                                                                                                                                                                                                                                                                                                         SAAQPAHQH-PPKHLARGTLKPAAHLVGDPSTPDSLRWRANT-----DRAFLR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                    STVQEKQQNISPLVRERGPQRVAAHITG-----TRGRSNTLSSPNSKNEKALGRKINS
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                                    VFFGAF
                                                                                                                                                   SSQYPFHVPLLSAQKSVCPGPQGPW-VRSVYQGAVFLLTQGDQLSTHTDGTPHLLLSPSS
                                                                                                                                                                                                                                                                     -----HGFL----LSNNSLLVPTSGLYFVYSQVVFSGEGCFPKATPTPLYLAHEVQLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tumor necrosis factor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 134.5;
Pred. No. 0.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:X57321; NID:g2137; PIDN:CAA40591.1; R;Pauli, U.; Beutler, B.; Peterhans, E. Gene 81, 185-191, 1989
A;Title: Porcine tumor necrosis factor alpha: Cloning with th A;Reference number: I46659; MUID:90034181; PMID:2478420
A;Accession: I46659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tumor necrosis factor alpha precursor - pig (;Species: Sus scrofa domestic a (domestic pig) C;Species: Sus scrofa domestica (domestic pig) C;Date: 10-Sep-199 #sequence revision 10-Sep-199 #text C;Accession: S12606; S17290; \overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\overline{\ov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              G;Superfamily: Lumor necrosis factor
G;Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine;
F;1-77/Domain: propeptide #status predicted <PRO>
F;78-232/Product: tumor necrosis factor alpha #status predicted <MAT>
F;19,20/Binding site: myristate (Lys) (covalent) #status predicted
F;81/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;144-176/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gene 102, 171-178, 1991
A,Title: The porcine tumor r
A,Reference number: S17289;
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 44-232 <PAU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Reference number: S18965
A; Accession: S18965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:X54859; NID:g2132; PIDN:CAA38639.1; A;Note: the authors translated the codon GAG for residue 202 R;Choi. C.S.; Molitor, T.W.; Lin, G.F.; Murtaugh, M.P. submitted to the EMBL Data Library, January 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-232 < KUH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R; Kuhnert, P.; Wuethrich,
Gene 102, 171-178, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:P23563; EMBL:X54001; NID:g2135; PIDN:CAA37949.1; PID:g2136
R;Kuhnert, P.; Wuethrich, C.; Peterhans, E.; Pauli, U.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-232 < DRE>
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A; Accession: S12606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Residues: 1-232 < CHO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Description: Complete nucleotide sequence of a cDNA encoding porcine tumor necrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: S17290
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                                                                                         DGLYLIYSQVLFRGQGCPSTNVFLTHTISRIA-----VSYQTKVNLLSAIKSPCQRETP
                                                                                                                                                                                                                                                                                                                                  --VIGPQKEEFPAGPL-
                                                                                                                                                                                                                                                                                                                                                                                      DSYMDPHDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                    AMMEVOGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKED
                                                                                                                                                                                                                                                                     VAAHITGTRGRSNTLSSPNS---KNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHE
                                                                                                                                                                                                          ----GLRSSSQTSDKPVAHVVANVKAEGQL--QWQSGYANALLANGVKLKDNQLVVPT
-DAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEAS-FFG 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9.0%;
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 133; DB 1;
Pred. No. 0.00082;
                                                                                                                                                   TKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSK--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 232;
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as Gly
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Indels 100;

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C;Genetics:
A;Gene: TNF-alpha
A;Introns: 62/3; 7;
A;Introns: 62/3; 7;
C;Superfamily: tum
C;Keywords: cytokii
F;78-234/Product: t
                                                                                                                                                                                                            R;Su, X.; Morris, D.D.; McGraw, R.A.
Gene 107, 319-321, 1991
A;Title: Cloning and characterization of gene TNP alpha encoding
A;Reference number: JQ1344; MUID:92084125; PMID:1748301
A;Accession: JQ1344
                                                                                                                                                                                                                                                                                                                                         tumor necrosis factor alpha precursor - horse
N;Alternate names: cachectin; TNF alpha
C;Species: Equus caballus (domestic horse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C/Keywords: glycoprotein; lipoprotein; myristylation; transmembrane F;19,20/Binding site: myristate (Lys) (covalent) #status predicted F;81/Binding site: carbohydrate (Ser) (covalent) #status predicted
                                                                                                                            A; Molecule type: DNA
A; Residues: 1-234 <SUX>
A; Residues: 1-234 <SUX>
A; Cross-references: UNIPROT: P29553; GB: M64087; NID: g164244; PIDN: ANA30959.1;
C; Comment: This protein is an important proximal mediator of endotoxemia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Sanjanwala, M.; Edwards, A. submitted to the EMBL Data Library, SA;Description: Baboon Tumor Necrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
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A; Residues: 1-233 <SAN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Species: Papio sp. (baboon);Date: 10-Sep-1999;Date: 10-Sep-1999;Bacession: S22052;Accession: S22052
Superfamily: tumor necrosis factor; Superfamily: tumor necrosis factor; Gly; Keywords: cytokine; cytotoxin; gly; 78-234/Product: tumor necrosis fac
                                                                                                                                                                                                                                                                                                                         Accession: JQ1344
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122 VAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGF
                                                                62/3; 79/1; 95/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 AMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        h 8.9%; Score 131.5; DB Similarity 19.2%; Pred. No. 0.0011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---DAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEAS-FFG 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EGAEAKPWYEPIYLGGVFQLEKGDRLSAEINLPDYLDFAESGQVYFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YLIYSQVLFKGQ------GCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYT-----SYPDPILLMKSARNSCWSK--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  precursor -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49; Mismatches
  glycoprotein; lipoprotein; lymphokine;
factor alpha #status predicted <TUM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -NPQAEGQL--QWLNRRANALLANGVELRDNQLVVPSEGL
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s Factor Derived
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                        macrophage;
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                        memb
                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Superfamily: tumor necrosis factor
C;Keywords: glycoprotein; lipoprotein; myristylation; transmembrane
F;20/Binding site: myristate (Lys) (covalent) #status predicted
F;81/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;145-177/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tumor necrosis factor alpha precursor - bovine (;Species: Bos primigenius taurus (cattle) C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Cludts, I.; Cleuter, Y.; Kettmann, R.; Burny, A.; Droogmans, Cytokine 5, 336-341, 1993
A;Title: Cloning and characterization of the tandemly arranged A;Reference number: 146046; MUID:94083525; PMID:8260599
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Gene: TNFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Cross-references: UNIPROT: Q06599;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-233 <CL2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Reference number: I46046; A; Accession: I46047
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F;82/Binding site: carbohydrate (Ser) (covalent)
F;146-178/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
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es 60; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                        VPADGLYLIYSQVLFRGQ-----GCPSTPLFLTHTISRIAVSYQTKVNILSAIKSPCHRE
                                                                IHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYK--YTSYPDPILLMKSARNSC---
                                                                                                                                                                                                 IGPQREESPGGP----SINSPLVQT------LRSSSQASS------
                                                                                                                                                                                                                                     ---KEDDSYMDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVR 115
                                                                                                                                                                                                                                                                                 LSEKAGGPQGSRSCLCLSLFSFLL----VAGATTLF--
                                                                                                                                                                                                                                                                                                                       MMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFL----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EDDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGP
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                                                                                                                                                       ERGPORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EEQL---PNAFQSIN-PLAQT------LRSSSRTPS------
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                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                      43;
                                                                                                                                                                                                                                                                                                                                                                   Score 130.5; DB
Pred. No. 0.0013;
3; Mismatches 9
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Pred. No. 0.0012;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL: Z14137; NID: g796; PIDN: CAA78511.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       - NPQAEGOL - - QWLSGRANALLANGVKLTDNQLVVPLD
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bovine lymphotoxin and

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276

181

130

Length

protein

PID:9798

Indels

93;

Gaps

13;

-CLLHFGV

55

180 230 175

85

125

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A;Title: Cloning and characterization of the tandemly arranged A;Reference number: I46046; MUID:94083525; PMID:8260599
A;Accession: I46046
                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 14
S24641
                                                                                                                                                             A;Molecule type: DNA
A;Residues: 1-204 <CL2>
A;Cross-references: UNIPROT:Q06600; EMBL:Z14137; NID:g796; PIDN:CAA78510.1; PID:g797
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CyAccession: I46046; S24641
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Immunogenetics 35, 351-353, 1992
A;Title: Sequence of the tumor necrosis factor/cachectin
A;Reference number: I54490; MUID:92218012; PMID:1348497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tumor necrosis factor alpha precursor - white-footed mouse C;Species: Peromyscus leucopus (white-footed mouse) C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-235 < RES>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPROT:P36939; GB:M59233; NID:g202506; PIDN:AAA40596.1; PID:g20250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Keywords: glycoprotein; lipoprotein; myristylation; 19,20/Binding site: myristate (Lys) (covalent) #st
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                                                        Query Match
Best Local
                                                                                                              Superfamily:
                                                                                                                                                 Genetics:
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                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        114 ALLANGMDLKDNQLVIPADGLYLVYSQVLFKGQ-----GCSSYVLLTHTVSRFAVSYEDK 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      110
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   99
                                                                                                                               32/3; 68/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45;
                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   site: carbohydrate
 TISTVQEKQQNISPLVRERGPQRVAAHITG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TPEWA-EAKPWYEPIYQGGVFQLEKGDRLSAEINLPDYLDYAESGQVYFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VNLLSAIKSPC-PKETPEGSELKPWYEPIYLGGVFQLEKGDRLSAEVNLPKYLDFAESGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SFLSN-LHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKY-TSYPDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IGPQREEKFPNNLP--IIGSMAQTLTLRSSSQNSSDKPVAHVVANHQVDEQLEWLSRGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ISPLVRERGPORVAAHITGTRGRSNTL-SSPNSKNEKALGRKINSWE-----SSRSGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---WSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEAS-FFG 276
                                                                                                              tumor necrosis factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81/1; 97/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8.8%;
larity 24.5%;
Conservative 39
                                        Conservative
                                                        8.6%;
24.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39;
                                    29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Lys)
(Ser)
                                    Score 127.5; DB 1;
Pred. No. 0.002;
9; Mismatches 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 129.5;
Pred. No. 0.0
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75;
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                                78;
   -TRGRSNTLSSPNSKNEKALGRKI
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                                                                       Length
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                                    Indels
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                                    35;
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                                  Gaps
   151
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N;Alternate names: cachectin; TNFA (;Species: Homo sapiens (man) (;Species: Homo sapiens (man) (;Species: Homo sapiens (man) (;Cache: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 09-Jul-2004 (;Accession: A93585; 336153; A93351; A44189; B61478; 153311; S62610; I54522; A01646; B23 R;Nedwin, G.E.; Naylor, S.L.; Sakaguchi, A.Y.; Smith, D.; Jarrett-Nedwin, J.; Pennica, D Nucleic Acids Res. 13, 6361-6373, 1985 Nucleic Acids Res. 13, 6361-6373, 1985 A;Title: Human lymphotoxin and tumor necrosis factor genes: structure, homology and chrc A;Reference number: A93585; MUID:86016093; PMID:2995927 A;Accession: A93585
                                                                   R;Marmenout, A.; Fransen, L.; Tavernier, J.; Van Der Heyden, J.; Tizard, R.; Eur. J. Blochem. 152, 515-522, 1985
A;Title: Molecular cloning and expression of human tumor necrosis factor and A;Reference number: 153311; MUID:86030296; PMID:3932069
A;Accession: 153311
                                                                                                                                                                                                                  A;Molecule type: protein
A;Molecule type: protein
A;Residues: 83-102;109-119;121-128,'X',130-131;142-144,'X',146,'XXX',150-152;159-174;180
A;Residues: 83-102;109-119;121-128,'X',130-131;142-144,'X',146,'XXX',150-152;159-174;180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:X02910; GB:X02159; NID:g37209; PIDN:CAA26669.1; PID:g37210
A;Note: this protein was isolated from the monocyte-like cell line HL-60 from a promyelo R;Wang, A.M.; Creasey, A.A.; Ladner, M.B.; Lin, L.S.; Strickler, J.; Van Arsdell, J.N.; Science 228, 149-154, 1985
A;Title: Molecular cloning of the complementary DNA for human tumor necrosis factor. A;Reference number: A44189; MUID:85142190; PMID:3856324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: Human tumour necrosis factor: precursor structure, expression A;Reference number: A93351; MUID:85086244; PMID:6392892 A;Accession: A93351
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A;Residues: I-233 <NED>
A;Cross-references: UNIPROT:P01375; GB:X02910; GB:X02159; NID:g37209; PIDN:CAA26669.1; P
A;Cross-references: UNIPROT:P01375; GB:X02910; GB:X02159; NID:g37209; PIDN:CAA26669.1; P
A;Iris, F.J.M.; Bougueleret, L.; Prieur, S.; Caterina, D.; Primas, G.; Perrot, V.; Jurka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ś
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                                   A;Status: translated from
                                                                                                                                                                                                                                                                                                                                                Lymphokine Res. 7, 175-185, 1988
A;Title: Simultaneous production of natural human tumor A;Reference number: A61478; MUID:88301617; PMID:2841543 A;Accession: B61478
                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:M10988; NID:g339737; PIDN:AAA61198.1; PID:g339738
R;Fukuda, S.; Ando, S.; Sanou, O.; Taniai, M.; Fujii, M.; Masaki, N.; Nakamura,
Lymphokine Res. 7, 175-185, 1988
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A; Residues: 1-62, 'S', 64-233 <WAN>
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A; Residues: 1-233 < PEN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R; Pennica, D.; Nedwin, G.I
Nature 312, 724-729, 1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:Z15026; NID:g37211; PIDN:CAA78745.1; PID:g37212
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1992
R;Pennica, D.; Nedwin, G.E.; Hayflick, J.S.; Seeburg, P.H.; Derynck, R.; Palladino,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: nucleic acid sequence not
A;Molecule type: DNA
A;Residues: 1-233 <IRI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: Dense Alu clustering and a potential new member of the NFkappaB family within A;Reference number: S36152; MUID:93272029; PMID:8499947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Iris, F.J.M.; Bougueleret, L. Nature Genet. 3, 137-145, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tumor necrosis factor alpha precursor [validated] - human
N;Alternate names: cachectin; TNFA
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A; Molecule type: DNA
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                                           GB/EMBL/DDBJ
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A;Map position: 6921.3-6921.3
A;Introns: 62/3; 78/1; 94/1
C;Complex: homotrimer
C;Superfamily: tumor necrosis factor
C;Superfamily: tumor necrosis factor
E;I-76/Domain: propeptide #status predicted <PRO>
F;I-7-233/Product: tumor necrosis factor #status experimental <MAT>
F;19,20/Binding site: myristate (Lys) (covalent) #status experimental
F;19,20/Binding site: carbohydrate (Ser) (covalent) (partial) #status experimental
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A;Contents: annotation; identification of myristylated lysines
R;Aggarwal, B.B.; Kohr, W.J.; Hass, P.E.; Moffat, B.; Spencer, S.A.; Henzel, W.J.; Bring
J. Biol. Chem. 260, 2345-2354, 1985
A;Title: Human tumor necrosis factor. Production, purification, and characterization.
A;Reference number: A92511; MUID:85130974; PMID:3871770
A;Contents: annotation; disulfide bond
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R;Takakura-Yamamoto, R.; Yamamoto, S.; Fukuda, S.; Kurimoto, M.
Eur. J. Biochem. 235, 431-437, 1996
A;Title: O-Glycosylated species of natural human tumor-necrosis factor-alpha.
A;Reference number: S62610; MUID:96202967; PMID:8631363
Search completed: March
Job time : 51 secs
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R;Stevenson, F.T.; Bursten, S.L.; Locksley, R.M.; Lovett, D.H.
J. Exp. Med. 176, 1053-1062, 1992
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Immunogenetics 39, 150-154, 1994
A;Title: A polymorphic variation in a putative regulation box
A;Reference number: 154522; MUID:94102809; PMID:7903959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GDB:120441; OMIM:191160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Gene: GDB: TNF; TNFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: protein
A; Residues: 77-99 < TAK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: S62610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;Accession: 154522; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 8.5%; Score 125.5; DB 1; Best Local Similarity 17.8%; Pred. No. 0.0036; Matches 51; Conservative 52; Mismatches 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;Residues: 1-8 <DAL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           145-177/Disulfide bonds: #status experimental
                                                                                                                            132
                                                                                                                                                                                                                                                                                                                    182 YYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYT-----SYPDPILLMKSARNSCWSK-- 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                   122 VAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGF 181
                                                                                                                                                                                                                                                                                                                                                                                       88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PVAHVVA------NPQAEGQL--QWLNRRANALLANGVELRDNQLVVPSEGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DSYMDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQR 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALPKKTGGPQGSRRCLFLSLFSFLIVAGATTLFCLLHFGVIGPQREEFPR-----
                                                                                                                                                                                                                                                        YLIYSQVLFKGQ------GCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETP
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